SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rge.

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rge.

start

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                          GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:         April 25, 2006, 09:55:26 ; Search time 1771 Seconds
                                           (without alignments)
                                           4012.101 Million cell updates/sec

Title:          US-10-088-319-2_COPY_331_455
Perfect score:  125
Sequence:       1 caaaaacaaaaaacctttac.........tgagtaaggtggccactttg 125

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                1:  gb_ba:*
                2:  gb_in:*
                3:  gb_env:*
                4:  gb_om:*
                5:  gb_ov:*
                6:  gb_pat:*
                7:  gb_ph:*
                8:  gb_pr:*
                9:  gb_ro:*
                10:  gb_sts:*
                11:  gb_sy:*
                12:  gb_un:*
                13:  gb_vi:*
                14:  gb_htg:*
                15:  gb_pl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	124	99.2	652	8	D50607	D50607 Human CD40
	2	124	99.2	1313	8	HUMCD40L5P	L47983 Homo sapien
	3	124	99.2	151978	14	CT005235	CT005235 Pan trogl
	4	124	99.2	175706	8	AL135783	AL135783 Human DNA
c	5	115	92.0	259175	14	AC106521	AC106521 Rattus no
	6	113.4	90.7	205673	14	AC124137	AC124137 Rattus no
	7	112	89.6	2395	6	AR350233	AR350233 Sequence
	8	112	89.6	2395	6	AR629955	AR629955 Sequence
	9	112	89.6	2395	6	AX351057	AX351057 Sequence
	10	112	89.6	6653	8	D31797	D31797 Homo sapien
	11	109.8	87.8	1878	4	AY333790	AY333790 Canis fam
	12	109.8	87.8	1878	6	BD211546	BD211546 Canine an
c	13	109.8	87.8	1878	6	BD211547	BD211547 Canine an
	14	109.8	87.8	1878	6	AR241524	AR241524 Sequence
c	15	109.8	87.8	1878	6	AR241525	AR241525 Sequence
	16	109.8	87.8	1878	6	AR254480	AR254480 Sequence
c	17	109.8	87.8	1878	6	AR254481	AR254481 Sequence
	18	100.8	80.6	213937	9	AL672128	AL672128 Mouse DNA
	19	97.8	78.2	2011	9	S71858S1	S71858 Mus musculu
	20	97	77.6	620	6	E09510	E09510 DNA encodin
	21	93.6	74.9	7057	6	AX251355	AX251355 Sequence
	22	93.6	74.9	7057	6	AX252056	AX252056 Sequence
	23	93.6	74.9	7057	6	AX281483	AX281483 Sequence
	24	93.6	74.9	7057	6	AX346750	AX346750 Sequence
	25	93.6	74.9	7057	6	AX348839	AX348839 Sequence
c	26	84.6	67.7	7057	6	AX251356	AX251356 Sequence
c	27	84.6	67.7	7057	6	AX252057	AX252057 Sequence
c	28	84.6	67.7	7057	6	AX281484	AX281484 Sequence
c	29	84.6	67.7	7057	6	AX346751	AX346751 Sequence
c	30	84.6	67.7	7057	6	AX348840	AX348840 Sequence
	31	37	29.6	37	6	AR629961	AR629961 Sequence
	32	37	29.6	37	6	AX351063	AX351063 Sequence
	33	34.2	27.4	200393	9	AC161601	AC161601 Mus muscu
c	34	34.2	27.4	206959	9	AC157917	AC157917 Mus muscu
c	35	33.6	26.9	226256	9	AC073599	AC073599 Mus muscu
c	36	33.6	26.9	233165	14	AC162370	AC162370 Mus muscu
	37	32.8	26.2	11435	1	U32753	U32753 Haemophilus
	38	32.8	26.2	110000	6	BD426631_07	Continuation (8 of
	39	32.8	26.2	110000	6	AR274513_07	Continuation (8 of
	40	32.8	26.2	110000	6	AR632719_07	Continuation (8 of
	41	32.2	25.8	184287	14	AC154708	AC154708 Mus muscu
	42	32.2	25.8	309506	9	AY363102S1	AY363102 Mus muscu
c	43	32	25.6	195169	9	AC108836	AC108836 Mus muscu
	44	31.6	25.3	242949	14	AC116255	AC116255 Rattus no
c	45	31.4	25.1	124964	8	AL159154	AL159154 Human DNA

ALIGNMENTS

RESULT 1
D50607

```
LOCUS       D50607                  652 bp    DNA     linear   PRI 10-FEB-1999
DEFINITION  Human CD40 ligand (hCD40L) gene, 5'-flanking region.
ACCESSION   D50607
VERSION     D50607.1  GI:849048
KEYWORDS    CD40 ligand; hCD40L; type-II membrane glycoprotein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   Seyama,K., Kira,S., Ishidoh,K., Souma,S., Miyakawa,T. and
            Kominami,E.
  TITLE     Genomic structure and PCR-SSCP analysis of the human CD40 ligand
            gene: its application to prenatal screening for X-linked hyper-IgM
            syndrome
  JOURNAL   Hum. Genet. 97 (2), 180-185 (1996)
   PUBMED   8566950
REFERENCE   2  (bases 1 to 652)
  AUTHORS   Ishidoh,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAY-1995) Kazumi Ishidoh, Juntendo University School
            of Medicine, Department of Biochemistry; 2-1-1 Hongo, Bunkyo-ku,
            Tokyo 113, Japan (Tel:03-5802-1031, Fax:03-5802-5889)
FEATURES             Location/Qualifiers
     source          1. .652
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /cell_type="lymphocyte and placenta"
     protein_bind    270. .285
                     /bound_moiety="NF-AT"
     protein_bind    315. .329
                     /bound_moiety="NF-AT"
     protein_bind    511. .516
                     /bound_moiety="NF-AT"
     TATA_signal     555. .563
     misc_feature    585
                     /note="transcription start site"
                     /evidence=experimental
     misc_feature    588
                     /note="transcription start site"
                     /evidence=experimental
     misc_feature    652
                     /note="translation start site"
ORIGIN

  Query Match             99.2%;  Score 124;  DB 8;  Length 652;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-29;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 521

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 581

Qy        122 TTTG 125
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```
Db        582 TTTG 585


RESULT 2
HUMCD40L5P
LOCUS       HUMCD40L5P              1313 bp    DNA     linear   PRI 06-FEB-2001
DEFINITION  Homo sapiens CD40 ligand gene, promoter and partial cds.
ACCESSION   L47983
VERSION     L47983.1  GI:1129041
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1313)
  AUTHORS   Schubert,L.A., King,G., Cron,R.Q., Lewis,D.B., Aruffo,A. and
            Hollenbaugh,D.
  TITLE     The human gp39 promoter. Two distinct nuclear factors of activated
            T cell protein-binding elements contribute independently to
            transcriptional activation
  JOURNAL   J. Biol. Chem. 270 (50), 29624-29627 (1995)
   PUBMED   8530342
REFERENCE   2  (bases 1 to 1313)
  AUTHORS   Schubert,L.A., King,G., Cron,R.Q., Lewis,D.B., Aruffo,A. and
            Hollenbaugh,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-DEC-1995) Dept of Pediatrics, Stanford University,
            300 Pasteur Drive CCSR Bldg Room 2115b, Stanford, CA 94305, USA
FEATURES             Location/Qualifiers
     source          1. .1313
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     promoter        <1. .1227
     mRNA            1228. .>1313
                     /product="CD40 ligand"
     5'UTR           1228. .1294
     CDS             1295. .>1313
                     /codon_start=1
                     /product="CD40 ligand"
                     /protein_id="AAC41932.1"
                     /db_xref="GI:1129042"
                     /translation="MIETYN"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.7e-29;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1164

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1224

Qy        122 TTTG 125
              ||||
Db       1225 TTTG 1228
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```
RESULT 3
CT005235
LOCUS       CT005235               151978 bp    DNA     linear   HTG 14-JUN-2005
DEFINITION  Pan troglodytes chromosome X clone RP43-015P08 map Xq28, ***
            SEQUENCING IN PROGRESS ***, 5 unordered pieces.
ACCESSION   CT005235
VERSION     CT005235.1  GI:67772562
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 151978)
  AUTHORS   Scheer,S., Kuhl,H., Kube,M., Mueller,I., Thiel,J., Borzym,K.,
            Klages,S., Sontag,M., Kosiura,A., Sudbrak,R., Beck,A., Lehrach,H.,
            Yaspo,M.L. and Reinhardt,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2005)
COMMENT     -------------- Genome Center
                 Center: Max-Planck-Institute for Molecular Genetics
                 Center code: MPIMG
            -------------- Project Information
                 Center clone name: RP43-015P08
            -------------- Summary Statistics
                 Sequencing vector: pUC19; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990329
                 Consensus quality: 149183 bases at least Q40
                 Consensus quality: 149379 bases at least Q30
                 Consensus quality: 149536 bases at least Q20
                 Quality coverage:  6.9
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest.
            --------------
            The RPCI-43 chimpanzee BAC library was prepared from DNA isolated
            from the blood of a single male chimpanzee using published
            protocols (Osoegawa,K. et al. Genomics 51:1-8). The DNA from the
            chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
            Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
            Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library
            characteristics are described at
            http://www.chori.org/bacpac/mchimp43.htm.
            The clone may be obtained from Pieter J. de Jong and coworkers
            (http://www.chori.org/bacpac).
            VECTOR:  pBACe3.
            contig 01          1. .14831
            contig 02      14932. .33675
            contig 03      33776. .60588
            contig 04      60689. .99409
            contig 05      99510. .151978.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
```

```
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    14831: contig of 14831 bp in length
            *    14832    14931: gap of unknown length
            *    14932    33675: contig of 18744 bp in length
            *    33676    33775: gap of unknown length
            *    33776    60588: contig of 26813 bp in length
            *    60589    60688: gap of unknown length
            *    60689    99409: contig of 38721 bp in length
            *    99410    99509: gap of unknown length
            *    99510   151978: contig of 52469 bp in length.
FEATURES             Location/Qualifiers
     source          1. .151978
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /chromosome="X"
                     /map="Xq28"
                     /clone="RP43-015P08"
     gap             14832. .14931
                     /estimated_length=unknown
     gap             33676. .33775
                     /estimated_length=unknown
     gap             60589. .60688
                     /estimated_length=unknown
     gap             99410. .99509
                     /estimated_length=unknown
ORIGIN

  Query Match             99.2%;  Score 124;  DB 14;  Length 151978;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-29;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129795 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 129854

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129855 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 129914

Qy        122 TTTG 125
              ||||
Db     129915 TTTG 129918


RESULT 4
AL135783
LOCUS       AL135783              175706 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP3-527F8 on chromosome Xq25-27.1
            Contains the TNFSF5 gene for tumor necrosis factor (ligand)
            superfamily (member 5 ,hyper-IgM syndrome), a novel gene, the 3'
            end of the ARHGEF6 gene for  Rac/Cdc42 guanine nucleotide exchange
            factor (GEF) 6 and a CpG island, complete sequence.
ACCESSION   AL135783
VERSION     AL135783.6  GI:6983480
KEYWORDS    HTG; ARHGEF6; TNFSF5.
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```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 175706)
  AUTHORS   Bird,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 16, 2000 this sequence version replaced gi:6983044.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome X, constructed by the Sanger Centre Chromosome X Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
            RP3-527F8 is from the library RPCI-3 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2.
FEATURES             Location/Qualifiers
     source          1. .175706
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="q25-27.1"
                     /clone="RP3-527F8"
                     /clone_lib="RPCI-3"
     gene            39996. .42685
                     /locus_tag="RP3-527F8.2-001"
     mRNA            join(39996. .40060,41030. .42685)
                     /locus_tag="RP3-527F8.2-001"
                     /product="novel protein"
                     /note="match: cDNAs: BC042469.1"
     CDS             41116. .41343
                     /locus_tag="RP3-527F8.2-001"
                     /standard_name="OTTHUMP00000024129"
                     /codon_start=1
                     /product="novel protein"
                     /protein_id="CAI42900.1"
                     /db_xref="GI:57208602"
                     /db_xref="UniProt/TrEMBL:Q5JVP7"
                     /translation="MSSSLWVLPHASSCTWNVFFPDPENSFRASSSRKSSLSLSPLHP
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                     HSFCMLPKSPALLYCGCLPSALWSTLAFVSP"
polyA_signal         42663. .42668
                     /locus_tag="RP3-527F8.2-001"
polyA_site           42685
                     /locus_tag="RP3-527F8.2-001"
gene                 join(48449. .48660,50522. .50653,54629. .54686,56612. .56674,
                     59295. .60646)
                     /gene="CD40LG"
                     /locus_tag="RP3-527F8.3-001"
mRNA                 join(48449. .48660,50522. .50653,54629. .54686,56612. .56674,
                     59295. .60646)
                     /gene="CD40LG"
                     /locus_tag="RP3-527F8.3-001"
                     /product="CD40 ligand (TNF superfamily, member 5,
                     hyper-IgM syndrome)"
                     /note="match: cDNAs: AF344841.1 AF344844.1 AF344859.1
                     AF344860.1 L07414.1 X67878.1 X68550.1 X96710.1 Z15017.1"
gene                 join(48483. .48660,50522. .50653,54629. .54686,59295. .60646)
                     /gene="CD40LG"
                     /locus_tag="RP3-527F8.3-002"
mRNA                 join(48483. .48660,50522. .50653,54629. .54686,59295. .60646)
                     /gene="CD40LG"
                     /locus_tag="RP3-527F8.3-002"
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                     hyper-IgM syndrome)"
                     /note="match: cDNAs: AF344853.1"
CDS                  join(48505. .48660,50522. .50653,54629. .54686,56612. .56674,
                     59295. .59671)
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                     /locus_tag="RP3-527F8.3-002"
                     /standard_name="OTTHUMP00000024130"
                     /note="match: proteins: P29965 P51749 Q9BDC7"
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                     /product="CD40 ligand (TNF superfamily, member 5,
                     hyper-IgM syndrome)"
                     /protein_id="CAI42901.1"
                     /db_xref="GI:57208603"
                     /db_xref="InterPro:IPR003263"
                     /db_xref="InterPro:IPR003636"
                     /db_xref="InterPro:IPR006052"
                     /db_xref="InterPro:IPR008983"
                     /translation="MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAV
                     YLHRRLDKIEDERNLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFVKDIMLNK
                     EETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQ
                     LTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPC
                     GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL"
CDS                  join(48505. .48660,50522. .50653,54629. .54686,59295. .59671)
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                     /locus_tag="RP3-527F8.3-002"
                     /standard_name="OTTHUMP00000024131"
                     /note="match: proteins: Q9BDM7"
                     /codon_start=1
                     /product="CD40 ligand (TNF superfamily, member 5,
                     hyper-IgM syndrome)"
                     /protein_id="CAI42902.1"
                     /db_xref="GI:57208604"
                     /translation="MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAV
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                     EASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFV
                     NVTDPSQVSHGTGFTSFGLLKL"
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polyA_signal    60626. .60631
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                /locus_tag="RP3-527F8.3-002"
polyA_site      60646
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                /locus_tag="RP3-527F8.3-002"
gene            complement(join(65803. .68425,69738. .69792,72276. .72375,
                75263. .75352,76880. .76973,78192. .78212,79791. .79916,
                80987. .81132,82146. .82224,83014. .83100,85933. .86079,
                88188. .88247,90866. .91004,107164. .107286,108931. .109026,
                113532. .113626,132358. .132428,143841. .144042,
                145479. .145603,147764. .147848,168669. .168883))
                /gene="ARHGEF6"
                /locus_tag="RP3-527F8.4-002"
mRNA            complement(join(65803. .68425,69738. .69792,72276. .72375,
                75263. .75352,76880. .76973,78192. .78212,79791. .79916,
                80987. .81132,82146. .82224,83014. .83100,85933. .86079,
                88188. .88247,90866. .91004,107164. .107286,108931. .109026,
                113532. .113626,132358. .132428,143841. .144042,
                145479. .145603,147764. .147848,168669. .168883))
                /gene="ARHGEF6"
                /locus_tag="RP3-527F8.4-002"
                /product="Rac/Cdc42 guanine nucleotide exchange factor
                (GEF) 6"
                /note="match: cDNAs: BC043505.1"
gene            complement(join(65803. .68425,69738. .69792,72276. .72375,
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                80987. .81132,82146. .82224,83014. .83100,85933. .86079,
                88188. .88247,90866. .91004,107164. .107286,108931. .109026,
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                145479. .145603,147764. .147848,167400. .167599))
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                /locus_tag="RP3-527F8.4-003"
                /product="Rac/Cdc42 guanine nucleotide exchange factor
                (GEF) 6"
                /note="match: ESTs: AU119513.1 BF791926.1 BG031451.1
                BG389231.1 BM479872.1 BM998736.1 BQ231848.1 BQ420871.1
                BU149436.1 CA405871.1"
gene            join(complement(AL683813.10:7264. .8634),
                complement(AL683813.10:5960. .6043),
                complement(147764. .147848),complement(145479. .145603),
                complement(143841. .144042),complement(132358. .132428),
                complement(113532. .113626),complement(108931. .109026),
                complement(107164. .107286),complement(90866. .91004),
                complement(88188. .88247),complement(85933. .86079),
                complement(83014. .83100),complement(82146. .82224),
                complement(80987. .81132),complement(79791. .79916),
                complement(78192. .78212),complement(76880. .76973),
                complement(75263. .75352),complement(72276. .72375),
                complement(69738. .69792),complement(65803. .68425))
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                /locus_tag="RP3-527F8.4-001"
mRNA            join(complement(AL683813.10:7264. .8634),
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                    complement(AL683813.10:5960. .6043),
                    complement(147764. .147848),complement(145479. .145603),
                    complement(143841. .144042),complement(132358. .132428),
                    complement(113532. .113626),complement(108931. .109026),
                    complement(107164. .107286),complement(90866. .91004),
                    complement(88188. .88247),complement(85933. .86079),
                    complement(83014. .83100),complement(82146. .82224),
                    complement(80987. .81132),complement(79791. .79916),

  Query Match             99.2%;  Score 124;  DB 8;  Length 175706;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-29;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48315 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 48374

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48375 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 48434

Qy        122 TTTG 125
              ||||
Db      48435 TTTG 48438


RESULT 5
AC106521/c
LOCUS       AC106521               259175 bp    DNA     linear   HTG 08-OCT-2002
DEFINITION  Rattus norvegicus clone CH230-29H24, *** SEQUENCING IN PROGRESS
            ***, 3 unordered pieces.
ACCESSION   AC106521
VERSION     AC106521.3  GI:22857484
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 259175)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 259175)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 259175)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Sep 14, 2002 this sequence version replaced gi:21731842.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information

```
            Center project name: GLCE
            Center clone name: CH230-29H24
          ---------- Summary Statistics
            Assembly program: Phrap; version 0.990329
            Consensus quality: 236111 bases at least Q40
            Consensus quality: 238370 bases at least Q30
            Consensus quality: 239565 bases at least Q20
            Estimated insert size: 259108; sum-of-contigs estimation
            Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
          ----------
          * NOTE: Estimated insert size may differ from sequence length
          *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
          * NOTE: This sequence may represent more than one clone.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 3 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *        1   254436: contig of 254436 bp in length
          *   254437   254536: gap of unknown length
          *   254537   256466: contig of 1930 bp in length
          *   256467   256566: gap of unknown length
          *   256567   259175: contig of 2609 bp in length.
FEATURES             Location/Qualifiers
     source          1. .259175
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-29H24"
     gap             254437. .254536
                     /estimated_length=unknown
     gap             256467. .256566
                     /estimated_length=unknown
ORIGIN

  Query Match             92.0%;  Score 115;  DB 14;  Length 259175;
  Best Local Similarity   95.9%;  Pred. No. 1.1e-26;
  Matches  118;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              |||| |||||||||||||||| |||||||||||| ||||||||||||||||||||||||
Db     124236 AAAAGAAAAAACCTTTACGTAACTTTTTTGCTGGGACAGAAGACTACGAAGCACATTTTC 124177

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACT 122
              ||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||
Db     124176 CAGGAAGTGTGGGTTGCGACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACT 124117

Qy        123 TTG 125
              |||
Db     124116 TTG 124114


RESULT 6
AC124137
LOCUS       AC124137               205673 bp    DNA     linear   HTG 20-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-285J20, WORKING DRAFT SEQUENCE.
ACCESSION   AC124137
VERSION     AC124137.4  GI:25139769
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KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 205673)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 205673)
AUTHORS Worley,K.C.
TITLE Direct Submission

```
  JOURNAL   Submitted (10-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 205673)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 20, 2002 this sequence version replaced gi:23269442.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: KABZ
                Center clone name: CH230-285J20
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 192345 bases at least Q40
                Consensus quality: 195056 bases at least Q30
                Consensus quality: 196514 bases at least Q20
                Estimated insert size: 198117; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   205673: contig of 205673 bp in length.
FEATURES            Location/Qualifiers
     source         1. .205673
                    /organism="Rattus norvegicus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10116"
                    /clone="CH230-285J20"
ORIGIN

  Query Match            90.7%;  Score 113.4;  DB 14;  Length 205673;
  Best Local Similarity  95.1%;  Pred. No. 3.9e-26;
  Matches  117;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              |||| |||||||||||||||| |||||||||| | ||||||||||||||||||||||||
Db       6740 AAAAGAAAAAACCTTTACGTAACTTTTTTGCTGGCACAGAAGACTACGAAGCACATTTTC 6799

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACT 122
              |||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db       6800 CAGGAAGTGTGGGTTGCGACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACT 6859

Qy        123 TTG 125
              |||
Db       6860 TTG 6862


RESULT 7
AR350233
LOCUS       AR350233               2395 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6586245.
ACCESSION   AR350233
VERSION     AR350233.1  GI:33751204
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2395)
  AUTHORS   Bennett,C.F., Baker,B.F., Wyatt,J. and Davis,S.E.
  TITLE     Antisense modulation of CD40 ligand expression
  JOURNAL   Patent: US 6586245-A 10 01-JUL-2003;
            ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES             Location/Qualifiers
     source          1. .2395
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.6%;  Score 112;  DB 6;  Length 2395;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-25;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 8
AR629955
LOCUS       AR629955               2395 bp    DNA     linear   PAT 14-FEB-2005
DEFINITION  Sequence 9 from patent US 6838556.
ACCESSION   AR629955
VERSION     AR629955.1  GI:59762089
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 2395)
  AUTHORS   Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
  TITLE     Promoters for regulated gene expression
  JOURNAL   Patent: US 6838556-A 9 04-JAN-2005;
            Genelabs Technologies, Inc.; Redwood City, CA
FEATURES             Location/Qualifiers
     source          1. .2395
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.6%;  Score 112;  DB 6;  Length 2395;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-25;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
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Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 9
AX351057
LOCUS       AX351057               2395 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 9 from Patent WO0194600.
ACCESSION   AX351057
VERSION     AX351057.1  GI:18616411
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Lim,M.Y. and Bruice,T.W.
  TITLE     Promoters for regulated gene expression
  JOURNAL   Patent: WO 0194600-A 9 13-DEC-2001;
            GENELABS TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .2395
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             89.6%;  Score 112;  DB 6;  Length 2395;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-25;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;
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Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872
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RESULT 10
D31797

LOCUS	D31797 6653 bp DNA linear PRI 23-OCT-2004
DEFINITION	Homo sapiens gene for CD40 ligand, complete cds.
ACCESSION	D31797 D31793 D31794 D31795 D31796
VERSION	D31797.2 GI:60391277
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Hollenbaugh,D., Grosmaire,L.S., Kullas,C.D., Chalupny,N.J., Braesch-Andersen,S., Noelle,R.J., Stamenkovic,I., Ledbetter,J.A. and Aruffo,A.
TITLE	The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity
JOURNAL	EMBO J. 11 (12), 4313-4321 (1992)
PUBMED	1385114
REFERENCE	2
AUTHORS	Spriggs,M.K., Armitage,R.J., Strockbine,L., Clifford,K.N., Macduff,B.M., Sato,T.A., Maliszewski,C.R. and Fanslow,W.C.
TITLE	Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion
JOURNAL	J. Exp. Med. 176 (6), 1543-1550 (1992)
PUBMED	1281209
REFERENCE	3
AUTHORS	Villa,A., Notarangelo,L., Disanto,J., Nacchi,P., Strina,D., Frattini,A., Lucchini,F., Patrosso,C., Giliani,S., Mantuano,E., Agosti,S., Nocera,G., Kroczek,R., Fischer,A., Ugazio,A., Basile,G. and Vezzoni,P.
TITLE	Organization of the human CD40L gene: implications for molecular defects in X chromosome-linked hyper-IgM syndrome and prenatal diagnosis
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (6), 2110-2114 (1994)
PUBMED	7907793
REFERENCE	4
AUTHORS	Shimadzu,M., Nunoi,H., Terasaki,H., Ninomiya,R., Iwata,M., Kanegasaka,S. and Matsuda,I.
TITLE	Structural organization of the gene for CD40 ligand: molecular analysis for diagnosis of X-linked hyper-IgM syndrome
JOURNAL	Biochim. Biophys. Acta 1260 (1), 67-72 (1995)
PUBMED	7999797
REFERENCE	5
AUTHORS	Shimadzu,M., Terasaki,H., Ninomiya,R., Shimizu,S., Nunoi,H. and Matsuda,I.

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  TITLE     Nucleotide sequence of CD40 ligand surrounding exon 5
  JOURNAL   Unpublished
REFERENCE   6  (bases 1 to 6653)
  AUTHORS   Shimadzu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUN-1994) Mitsunobu Shimadzu, Mitsubishi Yuka
            Bio-Clinical Laboratory, Inc., Genetics; Shimura 3-30-1, Itabashi,
            Tokyo, 174, Japan (Tel:81-3-5994-2432, Fax:81-3-5994-2940)
COMMENT     On or before Mar 1, 2005 this sequence version replaced gi:662386,
            gi:664885, gi:664886, gi:662387, gi:662388.
FEATURES             Location/Qualifiers
     source          1. .6653
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq26.3-27.1"
     protein_bind    677. .685
                     /bound_moiety="NF-kappaB"
     protein_bind    737. .743
                     /bound_moiety="NF-IL6"
     protein_bind    815. .819
                     /bound_moiety="GM-CSF"
     protein_bind    1040. .1045
                     /bound_moiety="alpha-INF2"
     enhancer        1188. .1195
                     /note="CRE2"
     enhancer        1209. .1216
                     /note="gamma-IRE"
     protein_bind    1291. .1295
                     /bound_moiety="GM-CSF"
     enhancer        1343. .1350
                     /note="gamma-IRE"
     enhancer        1359. .1366
                     /note="gamma-IRE"
     protein_bind    1397. .1403
                     /bound_moiety="AP-1"
     enhancer        1570. .1577
                     /note="gamma-IRE"
     protein_bind    1589. .1593
                     /bound_moiety="TCF1"
     misc_signal     1603. .1606
                     /note="GATA-1"
     protein_bind    1643. .1647
                     /bound_moiety="GM-CSF"
     enhancer        1689. .1696
                     /note="gamma-IRE"
     protein_bind    1701. .1705
                     /bound_moiety="TCF1"
     misc_signal     1731. .1736
                     /note="TATA like sequence"
     enhancer        1763. .1770
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     protein_bind    1803. .1807
                     /bound_moiety="GM-CSF"
     misc_feature    1840. .1862
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     protein_bind    1853. .1859
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     exon            1867. .2094
                     /product="CD40 ligand"
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                     /number=1
5'UTR                1867. .1938
                     /evidence=experimental
variation            1916
                     /note="polymorphism"
                     /citation=[1]
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                     5309. .5685)
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                     /protein_id="BAA06599.1"
                     /db_xref="GI:1518170"
                     /translation="MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAV
                     YLHRRLDKIEDERNLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFVKDIMLNK
                     EETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQ
                     LTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPC
                     GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL"
intron               2095. .>2395
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gap                  2396. .2495
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                     /number=1
exon                 2870. .3001
                     /product="CD40 ligand"
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intron               3002. .>3609
                     /number=2
gap                  3610. .3709
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intron               <3710. .4025
                     /number=2
exon                 4026. .4083
                     /product="CD40 ligand"
                     /number=3
intron               4084. .>4418
                     /number=3
gap                  4419. .4518
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intron               <4519. .4743
                     /number=3
exon                 4744. .4806
                     /product="CD40 ligand"
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intron               4807. .>4971
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gap                  4972. .5071
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intron               <5072. .5308
                     /number=4
exon                 5309. .6649
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misc_feature         6191. .6204
                     /note="C-rich sequence"
repeat_region        6375. .6418
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                     /evidence=experimental
     polyA_site      6649
ORIGIN

  Query Match             89.6%;  Score 112;  DB 8;  Length 6653;
  Best Local Similarity   99.2%;  Pred. No. 1.3e-25;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 11
AY333790
LOCUS       AY333790               1878 bp    mRNA    linear   MAM 20-JUL-2003
DEFINITION  Canis familiaris CD154 (CD154) mRNA, complete cds.
ACCESSION   AY333790
VERSION     AY333790.1  GI:32700006
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1878)
  AUTHORS   Yang,S. and Sim,G.-K.
  TITLE     Canine CD40 and CD40 Ligand cDNA Sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1878)
  AUTHORS   Yang,S. and Sim,G.-K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2003) Immunology, Heska Corporation, 1613
            Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES             Location/Qualifiers
     source          1. .1878
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     gene            1. .1878
                     /gene="CD154"
     5'UTR           1. .283
                     /gene="CD154"
     CDS             284. .1066
                     /gene="CD154"
                     /note="ligand for CD40"
                     /codon_start=1
                     /product="CD154"
                     /protein_id="AAP86654.1"
                     /db_xref="GI:32700007"
                     /translation="MIETYSQTAPRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAV
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                     AVKRQGLYYVYAQVTFCSNRAASSQAPFVASLCLHSPSGTERVLLRAASSRGSSKPCG
                     QQSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL"
     3'UTR           1067. .1878
                     /gene="CD154"
ORIGIN

  Query Match             87.8%;  Score 109.8;  DB 4;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 7.3e-25;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 12
BD211546
LOCUS       BD211546                1878 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same.
ACCESSION   BD211546
VERSION     BD211546.1  GI:33021316
KEYWORDS    JP 2002516104-A/52.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1878)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same
  JOURNAL   Patent: JP 2002516104-A 52 04-JUN-2002;
            HESKA CORP
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002516104-A/52
            PD   04-JUN-2002
            PF   28-MAY-1999 JP 2000551002
            PR   29-MAY-1998 US    60/087306
            PI   GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
              C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
            PC   A61K39/395,
            PC   A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
            PC   C07K14/54,
            PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
              G01N33/15,
            PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
            and feline immunoregulatory proteins, nucleic acid  CC
            molecules and
            CC   method of using the same
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
     source          1. .1878
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                     /db_xref="taxon:9615"
ORIGIN

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 7.3e-25;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 13
BD211547/c
LOCUS       BD211547                1878 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same.
ACCESSION   BD211547
VERSION     BD211547.1  GI:33021317
KEYWORDS    JP 2002516104-A/53.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1878)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same
  JOURNAL   Patent: JP 2002516104-A 53 04-JUN-2002;
            HESKA CORP
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002516104-A/53
            PD   04-JUN-2002
            PF   28-MAY-1999 JP 2000551002
            PR   29-MAY-1998 US    60/087306
            PI   GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
              C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
            PC   A61K39/395,
            PC   A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
            PC   C07K14/54,
            PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
              G01N33/15,
            PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
            and feline immunoregulatory proteins, nucleic acid  CC
            molecules and
            CC   method of using the same
            FH   Key             Location/Qualifiers
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            FT                   /organism='Canis familiaris (dog)'.
FEATURES             Location/Qualifiers
     source          1. .1878
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                     /db_xref="taxon:9615"
ORIGIN

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 7.3e-25;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
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Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662


RESULT 14
AR241524
LOCUS       AR241524               1878 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 64 from patent US 6471957.
ACCESSION   AR241524
VERSION     AR241524.1  GI:27287233
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1878)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 64 29-OCT-2002;
            Heska Corporation; Fort Collins, CO;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1878
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 7.3e-25;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
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Db        213 CTTTG 217


RESULT 15
AR241525/c
LOCUS       AR241525                1878 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 66 from patent US 6471957.
ACCESSION   AR241525
VERSION     AR241525.1  GI:27287234
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1878)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 66 29-OCT-2002;
            Heska Corporation; Fort Collins, CO;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1878
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 7.3e-25;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| |||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db       1786 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662


Search completed: April 25, 2006, 12:35:25
Job time : 1775 secs
```

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rng.

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rng.

start

Go Back to previous page

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 09:28:13 ; Search time 285 Seconds
(without alignments)
2923.111 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaaggtggccactttg 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	125	100.0	455	4	AAF74905	Aaf74905 Human alt
	2	124	99.2	455	4	AAF74904	Aaf74904 Human wil
	3	112	89.6	2395	6	ABK29860	Abk29860 Wild type
	4	112	89.6	2395	8	ACC44010	Acc44010 Human CD4
	5	109.8	87.8	1878	3	AAZ55534	Aaz55534 Canine CD
c	6	109.8	87.8	1878	3	AAZ55535	Aaz55535 Canine CD
	7	97	77.6	620	2	AAT05790	Aat05790 Human CD4
	8	93.6	74.9	7057	4	AAS46601	Aas46601 Tumour su
	9	93.6	74.9	7057	6	ABL33848	Abl33848 Human imm
	10	93.6	74.9	7057	6	ABL34594	Abl34594 Human met
	11	93.6	74.9	7057	6	ABL70407	Abl70407 Chemicall
	12	93.6	74.9	7057	6	AAS61354	Aas61354 Human gen
	13	93.6	74.9	7057	7	ADS99855	Ads99855 Bisulphit
c	14	84.6	67.7	7057	4	AAS46602	Aas46602 Tumour su
c	15	84.6	67.7	7057	6	ABL33849	Abl33849 Human imm
c	16	84.6	67.7	7057	6	ABL34595	Abl34595 Human met
c	17	84.6	67.7	7057	6	ABL70408	Abl70408 Chemicall
c	18	84.6	67.7	7057	6	AAS61355	Aas61355 Human gen
c	19	84.6	67.7	7057	7	ADS99856	Ads99856 Complemen
	20	37	29.6	37	6	ABK29866	Abk29866 CD40L -77
	21	32.8	26.2	110000	2	AAT42063_07	Continuation (8 of
	22	31.4	25.1	290040	14	ADV16961	Adv16961 Human pro
	23	31.4	25.1	290040	14	ADU92049	Adu92049 Human PAM
	24	31	24.8	438	4	AAI87513	Aai87513 Human pol
c	25	30.8	24.6	1470	3	AAC46273	Aac46273 Arabidops
c	26	30.8	24.6	1493	13	ADT15110	Adt15110 Plant cDN
c	27	30.4	24.3	454	5	ABV09654	Abv09654 Human pro
c	28	30.2	24.2	1833	10	ADD48377	Add48377 Human gen
c	29	30	24.0	7005	13	ADS47818	Ads47818 Bacterial
	30	29.8	23.8	2004	7	ADZ74714	Adz74714 Arabidops
c	31	29.8	23.8	52679	11	ACN44216	Acn44216 Mouse gen
	32	29.6	23.7	130312	14	AEB39168	Aeb39168 L. pneumo
c	33	29.6	23.7	143354	14	AEB42740	Aeb42740 L. pneumo
	34	29.4	23.5	1716	4	AAF61006	Aaf61006 P. putida
	35	29.4	23.5	5771	10	ADD45213	Add45213 Rat gene
	36	29.2	23.4	474	4	ABA59013	Aba59013 Human foe
	37	29.2	23.4	474	4	AAI38738	Aai38738 Probe #74
	38	29.2	23.4	474	4	AAK32932	Aak32932 Human bon
	39	29.2	23.4	474	4	AAK07183	Aak07183 Human bra
	40	29.2	23.4	474	4	ABS32660	Abs32660 Human liv
	41	29.2	23.4	474	6	ABS07737	Abs07737 Human gen
c	42	29.2	23.4	1474	3	AAC33070	Aac33070 Arabidops
	43	29.2	23.4	10929	13	ADT66569	Adt66569 Rat LutzP
	44	29.2	23.4	10929	14	ADX26167	Adx26167 Novel cel
c	45	28.8	23.0	5332	4	ABL29632	Abl29632 Drosophil

ALIGNMENTS

RESULT 1
AAF74905
ID AAF74905 standard; DNA; 455 BP.

XX
AC AAF74905;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human altered CD40L promoter sequence (A331C) SEQ ID NO:2.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Claim 1; Fig 2; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents the specifically claimed
CC altered human CD40L promoter sequence, from the present invention
XX
SQ Sequence 455 BP; 156 A; 72 C; 95 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 125; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 390

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 450

Qy        121 CTTTG 125
```

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                |||||
Db        451 CTTTG 455


RESULT 2
AAF74904
ID   AAF74904 standard; DNA; 455 BP.
XX
AC   AAF74904;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Human wild type CD40L promoter sequence SEQ ID NO:1.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 2; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents the wild type human CD40L
CC   promoter sequence, which is used in an example from the present invention
XX
SQ   Sequence 455 BP; 157 A; 71 C; 95 G; 132 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 124;  DB 4;  Length 455;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-34;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 391
```

```
Qy          62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         392 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 451

Qy         122 TTTG 125
               ||||
Db         452 TTTG 455


RESULT 3
ABK29860
ID   ABK29860 standard; DNA; 2395 BP.
XX
AC   ABK29860;
XX
DT   23-APR-2002  (first entry)
XX
DE   Wild type CD40Ln D1 promoter, nucleotides -1860 to +49.
XX
KW   Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW   HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW   vanH promoter; androgen receptor promoter; AR promoter;
KW   human epidermal growth factor receptor 2 promoter; her2 promoter;
KW   beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW   colon cancer; immunological disorder; prostate cancer; cytostatic;
KW   autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW   Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW   gene expression modulator; multiple sclerosis; MS;
KW   chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW   systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW   familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW   transgenic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194600-A2.
XX
PD   13-DEC-2001.
XX
PF   06-JUN-2001; 2001WO-US018343.
XX
PR   06-JUN-2000; 2000US-0209549P.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Kim JP,  Starr DB,  Tam AW,  Laurance ME,  Michelotti EF;
PI   Velligan MD,  Latour DR,  Thomas RL,  Kongpachith A,  Sheppard LT;
PI   Lim MY,  Bruice TW;
XX
DR   WPI; 2002-130595/17.
XX
PT   New nucleic acid regulatory sequences, which are able to regulate
PT   expression of a gene operably linked to a promoter, useful for regulating
PT   the expression of transgenes and for treating e.g., cancer and
PT   immunological diseases.
XX
PS   Example 2; Fig 5A-C; 95pp; English.
XX
CC   The invention describes an isolated nucleic acid regulatory sequence for
CC   a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
```

CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC (Bla) promoter. Transcription regulatory sequences may be used to
CC regulate expression of the endogenous, autologous or heterologous genes
CC operably linked to the promoter, and may be incorporated into
CC heterologous nucleic acid constructs for use in regulated expression of
CC transgenes. Regulated expression of cyclin D1 can be used in cancer
CC therapies, such as breast, colon or pancreatic cancers and familial
CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC may be used in the treatment of immunological disorders, such as
CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC arthritis. Regulated expression of genes under the control of the HBV
CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC hepatocellular carcinoma, and in the regulated expression of liver cell-
CC specific genes. Regulated expression of the vanH gene promoter can be
CC used in treatment of Enterococcus infection, while regulated expression
CC of the androgen receptor gene can be used in the treatment of prostate
CC cancer. This sequence represents the human CD40L promoter, nucleotides -
CC 1860 to +49, the regulatory regions of which are described in the method
CC of the invention
XX
SQ Sequence 2395 BP; 708 A; 453 C; 502 G; 732 T; 0 U; 0 Other;

Query Match 89.6%; Score 112; DB 6; Length 2395;
Best Local Similarity 99.2%; Pred. No. 1.6e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872
```

RESULT 4
ACC44010
ID ACC44010 standard; DNA; 2395 BP.
XX
AC ACC44010;
XX
DT 30-MAY-2003 (first entry)
XX
DE Human CD40 ligand gene fragment #1.
XX
KW ds; cytostatic; antiinflammatory; immunomodulator; antisense; gene;
KW gene therapy; human; CD40 ligand; phosphorothioate; 2'MOE wings; cancer;
KW autoimmune disorder; inflammatory disorder; apoptosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1939. .2094
FT /*tag= a

FT /product= "CD40 ligand fragment"
FT /note= "no stop codon given"
XX
PN WO2003008433-A1.
XX
PD 30-JAN-2003.
XX
PF 15-JUL-2002; 2002WO-US022635.
XX
PR 18-JUL-2001; 2001US-00909595.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Baker BF, Wyatt JR, Davis SE;
XX
DR WPI; 2003-239305/23.
DR P-PSDB; ABP98669.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding a CD40
PT ligand, useful in diagnostic and research applications, or for treating
PT diseases associated with expression of CD40 ligand, e.g. cancer or
PT autoimmune disorder.
XX
PS Example 13; Page 87-89; 108pp; English.
XX
CC The invention relates to novel antisense oligonucleotide targeted to the
CC human CD40 ligand gene. The oligonucleotides contain either
CC phosphorothioate internucleotide bonds replacing the usual phosphodiester
CC internucleotide bonds or have a peptide amide backbone replacing the
CC sugar phosphate backbone. The nucleotides flanking the central 10
CC nucleotides have 2'-methoxyethyl nucleotides (2'MOE wings) and the
CC cytidine nucleotides are all 5-methylcytidines. The antisense compounds
CC are useful for modulating the expression of CD40 ligand and for treating
CC diseases or conditions associated with expression of CD40 ligand, e.g.
CC cancer, autoimmune disorder, inflammatory disorder, or a disease or
CC condition arising from aberrant apoptosis. The antisense compounds are
CC also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent
CC or delay infection, inflammation or tumor formation, as research reagents
CC and kits, and in distinguishing between functions of various members of a
CC biological pathway. This sequence represents a fragment of the genomic
CC sequence encoding the human CD40 ligand. The sequence was used to design
CC the novel antisense oligonucleotides of the invention
XX
SQ Sequence 2395 BP; 708 A; 453 C; 502 G; 732 T; 0 U; 0 Other;

Query Match 89.6%; Score 112; DB 8; Length 2395;
Best Local Similarity 99.2%; Pred. No. 1.6e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872
```

```
RESULT 5
AAZ55534
ID   AAZ55534 standard; cDNA; 1878 BP.
XX
AC   AAZ55534;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Canine CD154 cDNA.
XX
KW   CD154; CD40 ligand; antibody; canine; feline; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             284. .1066
FT                   /*tag=  a
FT                   /product= "Canine CD154"
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G,  Yang S,  Dreitz MJ,  Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58215.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1f; Page 205-207; 264pp; English.
XX
CC   Sequences AAZ55533-Z55539 represent full-length or partial cDNAs encoding
CC   canine CD154 (CD40 ligand), while sequences AAZ55540-Z55545 represent
CC   feline CD154 cDNA sequences. The invention relates to canine interleukin-
CC   4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC   feline CD154, canine IL-5, canine IL-13, feline interferon-alpha (IFN-
CC   alpha) and feline granulocyte macrophage colony-stimulating factor
CC   (GMCSF), and nucleotides which encode these immunoregulatory proteins.
CC   The proteins, their associated nucleic acids, specific antibodies and
CC   inhibitors may be used as vaccines for therapeutic or prophylactic
CC   regulation of an immune response in animals (particularly cats, dogs,
CC   horses and humans). They may be used to treat autoimmune or infectious
CC   diseases including allergies, tumours, inflammation and graft rejection,
CC   and to increase the response from a co-administered antigen. The
CC   nucleotide sequences can also be used for the recombinant production of a
CC   protein, while nucleotide fragments are useful as probes, as
CC   amplification primers and as sources of inhibitory therapeutics (e.g.,
CC   antisense oligonucleotides). The proteins may be used to raise antibodies
CC   and to screen for modulators of activity, while the antibodies may be
CC   used in detection, and in drug targetting
XX
```

```
SQ   Sequence 1878 BP; 526 A; 461 C; 434 G; 457 T; 0 U; 0 Other;

  Query Match             87.8%;  Score 109.8;  DB 3;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 8.9e-29;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 6
AAZ55535/c
ID   AAZ55535 standard; cDNA; 1878 BP.
XX
AC   AAZ55535;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Canine CD154 cDNA complement.
XX
KW   CD154; CD40 ligand; antibody; canine; feline; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement(813. .1595)
FT                   /*tag=  a
FT                   /product= "Canine CD154"
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G,  Yang S,  Dreitz MJ,  Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58215.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1f; Page 209-210; 264pp; English.
XX
CC   Sequences AAZ55533-Z55539 represent full-length or partial cDNAs encoding
CC   canine CD154 (CD40 ligand), while sequences AAZ55540-Z55545 represent
```

CC feline CD154 cDNA sequences. The invention relates to canine interleukin-
CC 4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154, canine IL-5, canine IL-13, feline interferon-alpha (IFN-
CC alpha) and feline granulocyte macrophage colony-stimulating factor
CC (GMCSF), and nucleotides which encode these immunoregulatory proteins.
CC The proteins, their associated nucleic acids, specific antibodies and
CC inhibitors may be used as vaccines for therapeutic or prophylactic
CC regulation of an immune response in animals (particularly cats, dogs,
CC horses and humans). They may be used to treat autoimmune or infectious
CC diseases including allergies, tumours, inflammation and graft rejection,
CC and to increase the response from a co-administered antigen. The
CC nucleotide sequences can also be used for the recombinant production of a
CC protein, while nucleotide fragments are useful as probes, as
CC amplification primers and as sources of inhibitory therapeutics (e.g.,
CC antisense oligonucleotides). The proteins may be used to raise antibodies
CC and to screen for modulators of activity, while the antibodies may be
CC used in detection, and in drug targetting
XX
SQ Sequence 1878 BP; 457 A; 434 C; 461 G; 526 T; 0 U; 0 Other;

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
Best Local Similarity 97.6%; Pred. No. 8.9e-29;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| |||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1786 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662
```

RESULT 7
AAT05790
ID AAT05790 standard; DNA; 620 BP.
XX
AC AAT05790;
XX
DT 28-FEB-1996 (first entry)
XX
DE Human CD40 ligand exon 1 chromosomal DNA sequence.
XX
KW Exon; intron; chromosome; human CD40 ligand; PCR; amplifiifaction; primer;
KW probe; antisense; gene therapy; HIM syndrome; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 164. .319
FT /*tag= a
FT /product= "CD40 ligand a.a. 1-51"
FT /note= "exon 1"
FT intron 320. .620
FT /*tag= b
FT /cons_splice= 5'site:No, 3'site:Yes
FT /note= "This sequence only shows part of the 5' of the

```
FT                   intron sequence. The 3' splice site of the intron is
FT                   shown in AAT05791"
XX
PN   JP07163362-A.
XX
PD   27-JUN-1995.
XX
PF   25-NOV-1993;   93JP-00295102.
XX
PR   21-OCT-1993;   93JP-00263258.
XX
PA   (MITP ) MITSUBISHI YUKA BCL KK.
XX
DR   WPI; 1995-260044/34.
DR   P-PSDB; AAR80834.
XX
PT   Novel chromosomal DNA encoding a CD40 ligand and probes - useful for
PT   diagnosis and gene therapy of HIM syndrome.
XX
PS   Claim 1; Page 5-6; 14pp; Japanese.
XX
CC   The nucleotide sequence of exon 1 and surrounding 5' untranslated region
CC   and part of the 3' intron sequence from the chromosomal DNA sequence
CC   encoding the human CD40 ligand. The gene was isolated using an amplified
CC   fragment of the gene as a probe. The probe was a fragment amplified by
CC   the primers AAQ99758-9. The CD40 ligand primary gene is approx. 11 kb
CC   long and consists of 5 exons and 4 intron sequences (AAT05790-4). The
CC   sequence of the coding region was used to design a set of
CC   oligonucleotides (AAQ99760-73) which can be used as antisense probes for
CC   use in diagnosis and gene therapy of HIM syndrome
XX
SQ   Sequence 620 BP; 158 A; 138 C; 133 G; 191 T; 0 U; 0 Other;

  Query Match             77.6%;  Score 97;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-24;
  Matches   97;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         29 TTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACGATTGT 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACGATTGT 60

Qy         89 GCGCTCTTAACTAATCCTGAGTAAGGTGGCCACTTTG 125
              |||||||||||||||||||||||||||||||||||||
Db         61 GCGCTCTTAACTAATCCTGAGTAAGGTGGCCACTTTG 97


RESULT 8
AAS46601
ID   AAS46601 standard; DNA; 7057 BP.
XX
AC   AAS46601;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Tumour suppressor gene derived chemically modified sequence #323.
XX
KW   Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW   tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW   cytosine methylation; ds.
XX
OS   Homo sapiens.
```

XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
PS Claim 1; SEQ ID NO 323; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 4; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||  || ||||||||||||  | ||||  ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969
```

```
Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

RESULT 9
ABL33848
ID ABL33848 standard; DNA; 7057 BP.
XX
AC ABL33848;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1821.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 1821; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

```
  Query Match             74.9%;  Score 93.6;  DB 6;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 9.4e-23;
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;
```

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||| || |||||||||||| | |||| ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

```
RESULT 10
ABL34594
ID   ABL34594 standard; DNA; 7057 BP.
XX
AC   ABL34594;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human metastasis associated gene SEQ ID NO: 147.
XX
KW   Metastasis associated gene; cytostatic; gene therapy; cancer;
KW   cytosine methylation; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177376-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-EP003970.
XX
PR   06-APR-2000; 2000DE-01019058.
PR   07-APR-2000; 2000DE-01019173.
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-010922/01.
XX
PT   New nucleic acid derived from chemically treated metastasis genes, useful
PT   for diagnosis of cancers by analysis of cytosine methylation, also for
PT   treatment.
XX
PS   Claim 1; SEQ ID NO 147; 23pp + Sequence Listing; English.
XX
CC   The present invention provides a number of human metastasis associated
CC   genes which are modified by cytosine methylation. The sequences can be
CC   used in the diagnosis and treatment of cancer. The present sequence is
CC   one of the genes of the invention
XX
SQ   Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

  Query Match             74.9%;  Score 93.6;  DB 6;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 9.4e-23;
```

```
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||  || ||||||||||||  | ||||  ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973


RESULT 11
ABL70407
ID   ABL70407 standard; DNA; 7057 BP.
XX
AC   ABL70407;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Chemically treated cell signalling DNA sequence#149.
XX
KW   Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW   tumour; cytostatic; ds.
XX
OS   Unidentified.
XX
PN   WO200202807-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-EP007471.
XX
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-154758/20.
XX
PT   Nucleic acid, useful for diagnosis and therapy of diseases associated
PT   with cell signaling e.g. cancer, comprises chemically modified genomic
PT   sequences of genes associated with cell signaling.
XX
PS   Claim 1; SEQ ID NO 297; 24pp + Sequence Listing; English.
XX
CC   The invention relates to a nucleic acid comprising a sequence of at least
CC   18 bases of a segment of chemically pretreated DNA of genes associated
CC   with cell signalling. The activity of the modified sequences of the
CC   invention may be described as cytostatic. The object of the invention is
CC   to provide the chemically modified DNA of genes associated with cell
CC   signalling, as well as oligonucleotides and/or PNA-oligomers for
CC   detecting cytosine methylations, as well as a method which is
CC   particularly suitable for the diagnosis and/or therapy of genetic and
CC   epigenetic parameters of genes associated with cell signalling. The
CC   chemically modified DNA provided by the invention is useful for diagnosis
```

CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  ||||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||| || |||||||||||| | |||| ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

RESULT 12
AAS61354
ID AAS61354 standard; DNA; 7057 BP.
XX
AC AAS61354;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human gene regulation-associated gene oligonucleotide #309.
XX
KW Human; Gene regulation-associated gene; severe combined immunodeficiency;
KW cardiac damage; inflammatory response; Haemophilia; Werner syndrome;
KW asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
KW renal disease; Preeclampsia; cardiac allograft vascular disease;
KW colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
KW immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
KW nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200177375-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP003968.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX

DR WPI; 2002-017470/02.
XX
PT New nucleic acid sequences from chemically modified genes associated with
PT gene regulation, useful for analyzing cytosine methylations for diagnosis
PT and therapy of diseases e.g. severe combined immunodeficiency disease.
XX
PS Disclosure; SEQ ID NO 317; 26pp; English.
XX
CC The invention relates to 224 nucleic acid sequences comprising at least
CC 18 bases of a chemically pretreated gene associated with gene regulation
CC selected from 43 known genes (or complementary sequences). The chemical
CC pretreatment converts cytosine bases unmethylated at the 5-position to
CC uracil or another base with hybridisation behaviour dissimilar to
CC cytosine, to enable analysis of cytosine methylations. The DNA sequences,
CC oligomers (or sets/arrays) and method are useful in the diagnosis of
CC diseases (or predisposition to diseases) associated with gene regulation
CC and in therapy of such diseases, by enabling analysis of the cytosine
CC methylation patterns of such genes, kits are provided. They are
CC especially useful in diagnosis and therapy of e.g. severe combined
CC immunodeficiency disease, cardiac disorders, haemophilia, solid tumours
CC and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen
CC syndrome, renal disease, preeclampsia, graft versus-host disease. The
CC present sequence is a sequence included in the sequence data for this
CC specification and is associated with the human gene regulation-associated
CC genes. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               |||||||||||| || |||||||||||| | |||| ||||  |||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

RESULT 13
ADS99855
ID ADS99855 standard; DNA; 7057 BP.
XX
AC ADS99855;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bisulphite treated human gene associated with metastasis #74.
XX
KW Human; ds; gene; Bisulphite; metastasis; cancer; cytostatic;
KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;
KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
XX

OS Homo sapiens.
XX
PN US2003148327-A1.
XX
PD 07-AUG-2003.
XX
PF 21-JAN-2003; 2003US-00240485.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
PR 06-APR-2001; 2001WO-EP003970.
XX
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-010922/01.
XX
PT New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for
PT treatment.
XX
PS Claim 1; SEQ ID NO 147; 9pp; English.
XX
CC The invention relates to a nucleic acid comprising at least 18 bases from
CC a segment of the chemically pretreated DNA of genes associated with
CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any
CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are
CC the complements of SEQ ID 1,3,5, etc. Also included are an oligomer
CC (particularly an oligonucleotide or peptide nucleic acid) comprising at
CC least one base sequence of at least 9 bases which hybridises to (or is
CC identical with) the sequences referred to above, producing an array of
CC the oligomers on a carrier, obtaining genetic and/or epigenetic
CC parameters for diagnosis and/or therapy of diseases (or predisposition to
CC them) by analysis of cytosine methylation and a kit comprising a
CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the
CC method of above 5-unmethylated cytosines in a genomic DNA sample are
CC converted chemically to uracil, or another base with hybridisation
CC properties different from those of cytosine, then fragments of the
CC treated DNA amplified (particularly by polymerase chain reaction) using
CC the oligomers and a polymerase (preferably heat stable) to produce
CC labelled amplicons. These are tested for hybridisation to an array of
CC oligomers and any hybridisation detected. The amplicons are labelled with
CC fluorescent or radioactive markers, or with a detachable mass marker to
CC allow their detection by mass spectrometry, specifically using the matrix
CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.
CC To improve detection in the mass spectrometer, fragments formed in the
CC instrument have only a single net charge (positive or negative). The
CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-
CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that
CC are complementary to (or identical with) parts of the nuclei acids listed
CC above may be used as primers for amplification of the nucleic acids or
CC their complements, and for determining cytosine methylation status and/or
CC single nucleotide polymorphisms in metastasis-related genes. They can be
CC used for analysis of diseases associated with methylation of CpG
CC dinucleotides and to determine (epi)genetic parameters for diagnosis
CC and/or therapy of disease (or predisposition). The genomic DNA sequences

CC are useful for diagnosis and therapy of solid tumours and cancer. The
CC present sequence is a bisulphite treated human gene associated with
CC metastasis. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030148327.
XX
SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 7; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||| || |||||||||||| | |||| ||||  |||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

RESULT 14
AAS46602/c
ID AAS46602 standard; DNA; 7057 BP.
XX
AC AAS46602;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #324.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing

PT diseases associated with cytosine methylation state e.g. cancer.
XX
PS Claim 1; SEQ ID NO 324; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7057 BP; 2004 A; 51 C; 1259 G; 3743 T; 0 U; 0 Other;

Query Match 67.7%; Score 84.6; DB 4; Length 7057;
Best Local Similarity 80.5%; Pred. No. 1.6e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||  ||   | | || |||||||| ||||||||
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Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
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Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
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Db       2088 TTT 2086
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RESULT 15
ABL33849/c
ID ABL33849 standard; DNA; 7057 BP.
XX
AC ABL33849;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1822.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 1822; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 7057 BP; 2004 A; 51 C; 1259 G; 3743 T; 0 U; 0 Other;

Query Match 67.7%; Score 84.6; DB 6; Length 7057;
Best Local Similarity 80.5%; Pred. No. 1.6e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db       2208 AAAAACAAAAAACCTTTACGTAACGTTTTTACTAAAAAAAAAAACTACGAAACACATTTT 2149

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||  || | |   || |||||||| | |||||||||||||||| | |||  |  ||||
Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
              |||
Db       2088 TTT 2086
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Search completed: April 25, 2006, 10:12:51
Job time : 287 secs

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rni.

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rni.

start

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 10:13:01 ; Search time 104 Seconds
(without alignments)
2136.492 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaaggtggccactttg 125

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
	1	112	89.6	2395	3	US-09-909-595-10	Sequence 10, Appl
	2	112	89.6	2395	3	US-09-875-453B-9	Sequence 9, Appli
	3	109.8	87.8	1878	3	US-09-322-409-64	Sequence 64, Appl
c	4	109.8	87.8	1878	3	US-09-322-409-66	Sequence 66, Appl
	5	109.8	87.8	1878	3	US-09-451-527-64	Sequence 64, Appl
c	6	109.8	87.8	1878	3	US-09-451-527-66	Sequence 66, Appl
	7	37	29.6	37	3	US-09-875-453B-15	Sequence 15, Appl
	8	32.8	26.2	1830121	3	US-09-557-884-1	Sequence 1, Appli
	9	32.8	26.2	1830121	3	US-09-643-990A-1	Sequence 1, Appli
	10	32.8	26.2	1830121	3	US-10-158-865-1	Sequence 1, Appli
c	11	28.8	23.0	340380	3	US-09-949-016-14179	Sequence 14179, A
	12	28.6	22.9	894	3	US-09-248-796A-1443	Sequence 1443, Ap
	13	28.4	22.7	74790	3	US-09-949-016-15321	Sequence 15321, A
	14	28.2	22.6	1746	3	US-09-107-532A-3181	Sequence 3181, Ap
	15	28.2	22.6	126254	3	US-09-949-016-15341	Sequence 15341, A
	16	28	22.4	948	3	US-09-252-991A-10169	Sequence 10169, A
	17	27.8	22.2	36203	3	US-09-949-016-15430	Sequence 15430, A
	18	27.6	22.1	754	3	US-09-640-211A-511	Sequence 511, App
	19	27.4	21.9	385136	3	US-09-949-016-16073	Sequence 16073, A
	20	27.2	21.8	601	3	US-09-949-016-132413	Sequence 132413,
c	21	27.2	21.8	2327	3	US-09-071-709-5	Sequence 5, Appli
c	22	27.2	21.8	2327	3	US-09-713-669-5	Sequence 5, Appli
	23	27.2	21.8	450395	3	US-09-949-016-15473	Sequence 15473, A
c	24	27	21.6	470	3	US-09-621-976-10700	Sequence 10700, A
	25	27	21.6	876	3	US-09-328-352-1291	Sequence 1291, Ap
	26	27	21.6	151256	3	US-09-949-016-12674	Sequence 12674, A
	27	27	21.6	151261	3	US-09-949-016-13242	Sequence 13242, A
	28	26.8	21.4	700	3	US-09-735-271-1292	Sequence 1292, Ap
c	29	26.8	21.4	54550	3	US-10-327-189-42	Sequence 42, Appl
	30	26.6	21.3	374	3	US-09-640-211A-1599	Sequence 1599, Ap
	31	26.6	21.3	601	3	US-09-949-016-203482	Sequence 203482,
	32	26.6	21.3	601	3	US-09-949-016-203483	Sequence 203483,
	33	26.6	21.3	936	3	US-09-710-279-1247	Sequence 1247, Ap
	34	26.6	21.3	999	3	US-09-134-001C-1195	Sequence 1195, Ap
	35	26.6	21.3	1365	3	US-09-134-001C-1601	Sequence 1601, Ap
c	36	26.6	21.3	3238	3	US-09-710-279-4150	Sequence 4150, Ap
c	37	26.6	21.3	3497	3	US-09-710-279-3617	Sequence 3617, Ap
	38	26.6	21.3	37565	3	US-09-949-016-15847	Sequence 15847, A
	39	26.6	21.3	56976	3	US-09-949-016-17486	Sequence 17486, A
	40	26.6	21.3	101674	3	US-09-949-016-12033	Sequence 12033, A
	41	26.4	21.1	1382	3	US-09-270-767-15211	Sequence 15211, A
	42	26.4	21.1	7885	3	US-09-555-367A-3	Sequence 3, Appli
c	43	26.4	21.1	9062	3	US-08-956-171E-85	Sequence 85, Appl
c	44	26.4	21.1	9062	3	US-08-781-986A-85	Sequence 85, Appl
	45	26.4	21.1	13875	2	US-08-734-344-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-909-595-10
; Sequence 10, Application US/09909595
; Patent No. 6586245
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Scott E. Davis
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
;  FILE REFERENCE: RTS-0223
;  CURRENT APPLICATION NUMBER: US/09/909,595
;  CURRENT FILING DATE:  2001-07-18
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
;   LENGTH: 2395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1939)...(2094)
US-09-909-595-10

  Query Match             89.6%;  Score 112;  DB 3;  Length 2395;
  Best Local Similarity   99.2%;  Pred. No. 2.2e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 2
US-09-875-453B-9
; Sequence 9, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jungsuh P.
;  APPLICANT:  Starr, Douglas B.
;  APPLICANT:  Tam, Albert W.
;  APPLICANT:  Laurance, Megan E.
;  APPLICANT:  Michelotti, Emil F.
;  APPLICANT:  Velligan, Mark D.
;  APPLICANT:  Latour, Derek R.
;  APPLICANT:  Thomas, Rita L.
;  APPLICANT:  Kongpachith, Ana
;  APPLICANT:  Sheppard, Liana T.
;  APPLICANT:  Lim, Moon Young
;  APPLICANT:  Bruice, Thomas W.
;  TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
;  FILE REFERENCE: 54600-8135.US00
;  CURRENT APPLICATION NUMBER: US/09/875,453B
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,549
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 2395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-875-453B-9
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  Query Match             89.6%;  Score 112;  DB 3;  Length 2395;
  Best Local Similarity   99.2%;  Pred. No. 2.2e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
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Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 3
US-09-322-409-64
; Sequence 64, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT: Yang, Shumin
;  APPLICANT: Dreitz, Matthew J.
;  APPLICANT: Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C1
;  CURRENT APPLICATION NUMBER: US/09/322,409
;  CURRENT FILING DATE: 1999-05-28
;  EARLIER APPLICATION NUMBER: 60/087,306
;  EARLIER FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (284)..(1063)
US-09-322-409-64

  Query Match             87.8%;  Score 109.8;  DB 3;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-30;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217
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RESULT 4
US-09-322-409-66/c
; Sequence 66, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT: Yang, Shumin
;  APPLICANT: Dreitz, Matthew J.
;  APPLICANT: Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C1
;  CURRENT APPLICATION NUMBER: US/09/322,409
;  CURRENT FILING DATE: 1999-05-28
;  EARLIER APPLICATION NUMBER: 60/087,306
;  EARLIER FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-322-409-66

  Query Match             87.8%;  Score 109.8;  DB 3;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-30;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||||  ||||||||||||||||||||||||||||||||||
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Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662


RESULT 5
US-09-451-527-64
; Sequence 64, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT: Yang, Shumin
;  APPLICANT: Dreitz, Matthew J.
;  APPLICANT: Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C2
;  CURRENT APPLICATION NUMBER: US/09/451,527
;  CURRENT FILING DATE: 1999-12-01
;  EARLIER APPLICATION NUMBER: 09/322,409
;  EARLIER FILING DATE: 1999-05-28
;  EARLIER APPLICATION NUMBER: 60/087,306
;  EARLIER FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 174
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (284)..(1063)
US-09-451-527-64

  Query Match             87.8%;  Score 109.8;  DB 3;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-30;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 6
US-09-451-527-66/c
; Sequence 66, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT: Yang, Shumin
;  APPLICANT: Dreitz, Matthew J.
;  APPLICANT: Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C2
;  CURRENT APPLICATION NUMBER: US/09/451,527
;  CURRENT FILING DATE: 1999-12-01
;  EARLIER APPLICATION NUMBER: 09/322,409
;  EARLIER FILING DATE: 1999-05-28
;  EARLIER APPLICATION NUMBER: 60/087,306
;  EARLIER FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-451-527-66

  Query Match             87.8%;  Score 109.8;  DB 3;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-30;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db       1786 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727
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Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662


RESULT 7
US-09-875-453B-15
; Sequence 15, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jungsuh P.
;  APPLICANT:  Starr, Douglas B.
;  APPLICANT:  Tam, Albert W.
;  APPLICANT:  Laurance, Megan E.
;  APPLICANT:  Michelotti, Emil F.
;  APPLICANT:  Velligan, Mark D.
;  APPLICANT:  Latour, Derek R.
;  APPLICANT:  Thomas, Rita L.
;  APPLICANT:  Kongpachith, Ana
;  APPLICANT:  Sheppard, Liana T.
;  APPLICANT:  Lim, Moon Young
;  APPLICANT:  Bruice, Thomas W.
;  TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
;  FILE REFERENCE: 54600-8135.US00
;  CURRENT APPLICATION NUMBER: US/09/875,453B
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,549
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-875-453B-15

  Query Match             29.6%;  Score 37;  DB 3;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         47 TACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACG 83
              |||||||||||||||||||||||||||||||||||||
Db          1 TACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACG 37


RESULT 8
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
;   GENERAL INFORMATION:
;        APPLICANT: Fleischmann et al.
;        TITLE OF INVENTION: The Nucleotide sequence of
;                            the Haemophilus influenzae Rd Genome, Fragments
;                            Thereof, and Uses Thereof
;        NUMBER OF SEQUENCES: 1
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
```

```
;              STREET: 9410 Key West Avenue
;              CITY: Rockville
;              STATE: MD
;              COUNTRY: USA
;              ZIP: 20850
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: 3 1/2 inch diskette
;              COMPUTER: Dell Pentium
;              OPERATING SYSTEM: MS DOS v6.22
;              SOFTWARE: ASCII Text
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/557,884
;              FILING DATE: 25-Apr-2000
;              CLASSIFICATION:
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/476,102
;              FILING DATE: JUN-5-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Michelle S. Marks
;              REGISTRATION NUMBER: 41,971
;              REFERENCE/DOCKET NUMBER: PB186P3
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 301-309-8504
;              TELEFAX: 301-309-8439
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1830121 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

  Query Match             26.2%;  Score 32.8;  DB 3;  Length 1830121;
  Best Local Similarity   55.2%;  Pred. No. 1.1;
  Matches   64;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              ||||||||  || |     ||  | | |  |||||   ||| | | |  | || || | |
Db     754880 AAAACAAAGTACTTGGCTTTATTGATGTACCTGGGCACGAAAAATTCTTATCAAATATGC 754939

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGC 118
                | | || | ||  ||    ||| |||  | |||| |    ||| | | |  |||
Db     754940 TGGCAGGTTTAGGTGGCGTGCATTATGCAATGTTAATTGTGGCTGCGGATGAAGGC 754995


RESULT 9
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
;   GENERAL INFORMATION:
;         APPLICANT: Robert D. Fleischmann
;                    Mark D. Adams
;                    Owen White
;                    Hamilton O. Smith
;                    J. Craig Venter
;         TITLE OF INVENTION: The Nucleotide sequence of
;                             the Haemophilus influenzae Rd Genome, Fragments
;                             Thereof, and Uses Thereof
;         NUMBER OF SEQUENCES: 1
;         CORRESPONDENCE ADDRESS:
```

```
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville,
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3 1/2 inch diskette
;             COMPUTER: Dell Pentium
;             OPERATING SYSTEM: MS DOS v6.22
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/643,990A
;             FILING DATE: 23-Aug-2000
;             CLASSIFICATION:
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/487,429
;             FILING DATE: 1995-06-07
;             APPLICATION NUMBER: 08/426,787
;             FILING DATE: 1995-04-21
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kenley K. Hoover
;             REGISTRATION NUMBER: 40,302
;             REFERENCE/DOCKET NUMBER: PB186P1C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-610-5790
;             TELEFAX: 310-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1830121 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

  Query Match             26.2%;  Score 32.8;  DB 3;  Length 1830121;
  Best Local Similarity   55.2%;  Pred. No. 1.1;
  Matches   64;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              ||||||||  || |     ||  | | |  |||||   ||| | | |  | || || | |
Db     754880 AAAACAAAGTACTTGGCTTTATTGATGTACCTGGGCACGAAAAATTCTTATCAAATATGC 754939

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGC 118
                | | || | ||  ||    ||| |||  | |||| |   .||| | | |  |||
Db     754940 TGGCAGGTTTAGGTGGCGTGCATTATGCAATGTTAATTGTGGCTGCGGATGAAGGC 754995


RESULT 10
US-10-158-865-1
; Sequence 1, Application US/10158865
; Patent No. 6846651
; GENERAL INFORMATION:
;  APPLICANT: Fleischmann et al.
;  TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fr
; Patent No. 6846651
;  TITLE OF INVENTION:  Thereof, and Uses Thereof
;  FILE REFERENCE: PB186P2C1D1
;  CURRENT APPLICATION NUMBER: US/10/158,865
;  CURRENT FILING DATE:  2002-06-03
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;  PRIOR APPLICATION NUMBER: US 09/557,884
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 08/476,102
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: US 08/426,787
;  PRIOR FILING DATE: 1995-04-21
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1830121
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4747)..(4747)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9921)..(9921)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10150)..(10150)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (29298)..(29298)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (36543)..(36543)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (36551)..(36551)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (36636)..(36636)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (40808)..(40810)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (44416)..(44416)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (44905)..(44905)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (44975)..(44975)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (45593)..(45593)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
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;    NAME/KEY: misc_feature
;    LOCATION: (45732)..(45732)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (47036)..(47036)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (51334)..(51334)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (51602)..(51602)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (51786)..(51786)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (51805)..(51805)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (55369)..(55369)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (65309)..(65309)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (65313)..(65313)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (80024)..(80024)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (100091)..(100091)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (102696)..(102696)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (105121)..(105121)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (107248)..(107248)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (117136)..(117136)
;    OTHER INFORMATION: n equals a,t,c, or g
;    FEATURE:
;    NAME/KEY: misc_feature
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;   LOCATION: (119750)..(119750)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119924)..(119924)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (120038)..(120038)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (121344)..(121344)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (122167)..(122167)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (122336)..(122336)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (131340)..(131340)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (131360)..(131360)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (139910)..(139910)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (140398)..(140398)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142750)..(142750)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145058)..(145058)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145171)..(145171)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145942)..(145942)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (147197)..(147197)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (150841)..(150841)
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;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152500)..(152500)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature

  Query Match             26.2%;  Score 32.8;  DB 3;  Length 1830121;
  Best Local Similarity   55.2%;  Pred. No. 1.1;
  Matches   64;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              ||||||||  || |     ||  | | |  |||||   ||| | | |  | || || | |
Db     754880 AAAACAAAGTACTTGGCTTTATTGATGTACCTGGGCACGAAAAATTCTTATCAAATATGC 754939

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGC 118
                | | || | ||  ||    ||| |||  | |||| |    ||| | | |  |||
Db     754940 TGGCAGGTTTAGGTGGCGTGCATTATGCAATGTTAATTGTGGCTGCGGATGAAGGC 754995


RESULT 11
US-09-949-016-14179/c
; Sequence 14179, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14179
;   LENGTH: 340380
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(340380)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14179

  Query Match             23.0%;  Score 28.8;  DB 3;  Length 340380;
  Best Local Similarity   54.8%;  Pred. No. 17;
  Matches   57;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| ||||| | || |    |||| |  | | |||| |  |      | | || | ||
Db      73536 AAACACAAACAGCCCTCGGATAACCTGATGGGTGGGTGTCACTGACTCCAGGCCCCTTGC 73477

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |||||||||    |||     |  ||||| || |      ||||
Db      73476 CCAGGAAGTTCCTGCTTTCCTGCCTGTGCCCTGTCCCTCTATCC 73433
```

RESULT 12
US-09-248-796A-1443
; Sequence 1443, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1443
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1443

Query Match 22.9%; Score 28.6; DB 3; Length 894;
Best Local Similarity 59.0%; Pred. No. 1.7;
Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
Qy         23 AACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAAC 82
              || |||     |   | |||| ||||   |||  | || |||  |||  | |||    |
Db        355 AAAGTTAGACATTATATAGAAAACTATCTAGCCAAGTTCCCAAAAAGACTTGGCGATGAT 414

Qy         83 GATTGTGCGCTCTTAACTAATCC 105
              ||| |  ||||| || |||| ||
Db        415 GATAGGTCGCTCCTAGCTAAACC 437
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RESULT 13
US-09-949-016-15321
; Sequence 15321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15321
; LENGTH: 74790
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15321

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  Query Match             22.7%;  Score 28.4;  DB 3;  Length 74790;
  Best Local Similarity   56.4%;  Pred. No. 13;
  Matches   53;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          6 ACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAG 65
              | ||  ||    |  | ||   |   | || |||||||| ||| |||| | |||||||||
Db      27003 ATAACTAAGTGATTAGCAAAACTAGAGTTGTGAGAGAAGTCTATGAAGAATATTTTCCAG 27062

Qy         66 GAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC 99
                 || |  | |  |   ||  | |  | ||| |
Db      27063 AGTGTTTTTGTTTTATAAATATTTCATTTTTAGC 27096


RESULT 14
US-09-107-532A-3181
; Sequence 3181, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM:
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3181:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1746 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
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```
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...1746
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
US-09-107-532A-3181

  Query Match             22.6%;  Score 28.2;  DB 3;  Length 1746;
  Best Local Similarity   54.3%;  Pred. No. 3.1;
  Matches   57;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy         20 CGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGC 79
              || ||||  ||| |    |   |||| | |  || |||||| ||| |    ||| | |
Db        658 CGAAACGGATTTCCGCAAATCAAAGAATTCTCAGAACATTTTTCAGTTCCTGTTGTCGCT 717

Qy         80 AACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACTTT 124
                || |   ||      || || ||||||  |   ||   |||||
Db        718 TCCGTTCTAGCAAAAGGAATTATTCCTGATGATTATGAAAACTTT 762


RESULT 15
US-09-949-016-15341
; Sequence 15341, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15341
;   LENGTH: 126254
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126254)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15341

  Query Match             22.6%;  Score 28.2;  DB 3;  Length 126254;
  Best Local Similarity   61.6%;  Pred. No. 19;
  Matches   45;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||||  ||||| || | | ||| | | |   |  || ||||   |   ||  | ||||
Db     122450 CAAAAAACAAAAAACTGTTCTTAATGGTGTGAGTTAGAAAGAACGTTTTAAAAAAAATTT 122509

Qy         61 TCCAGGAAGTGTG 73
              |    ||||||||
Db     122510 TTTTAGAAGTGTG 122522
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Search completed: April 25, 2006, 10:53:51
Job time : 107 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rnpbm.

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start

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 10:52:12 ; Search time 430 Seconds
(without alignments)
2403.889 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaaggtggccactttg 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.		Score	Query Match	Length	DB	ID	Description
1		112	89.6	2395	3	US-09-875-453-9	Sequence 9, Appli
2		112	89.6	2395	3	US-09-909-595-10	Sequence 10, Appl
3		112	89.6	2395	8	US-10-484-007-10	Sequence 10, Appl
4		109.8	87.8	1878	5	US-10-218-654-64	Sequence 64, Appl
5	c	109.8	87.8	1878	5	US-10-218-654-66	Sequence 66, Appl
6		109.8	87.8	1878	6	US-10-262-439-64	Sequence 64, Appl
7	c	109.8	87.8	1878	6	US-10-262-439-66	Sequence 66, Appl
8		93.6	74.9	7057	6	US-10-311-455-1821	Sequence 1821, Ap
9		93.6	74.9	7057	6	US-10-240-485-147	Sequence 147, App
10		93.6	74.9	7057	7	US-10-221-613-317	Sequence 317, App
11		93.6	74.9	7057	7	US-10-221-714A-323	Sequence 323, App
12	c	84.6	67.7	7057	6	US-10-311-455-1822	Sequence 1822, Ap
13	c	84.6	67.7	7057	6	US-10-240-485-148	Sequence 148, App
14	c	84.6	67.7	7057	7	US-10-221-613-318	Sequence 318, App
15	c	84.6	67.7	7057	7	US-10-221-714A-324	Sequence 324, App
16		37	29.6	37	3	US-09-875-453-15	Sequence 15, Appl
17		32.8	26.2	1830121	7	US-10-329-670-1	Sequence 1, Appli
18		32.8	26.2	1830121	8	US-10-158-865-1	Sequence 1, Appli
19		32.8	26.2	1830121	9	US-10-981-687-1	Sequence 1, Appli
20		31.4	25.1	290040	8	US-10-850-591-3	Sequence 3, Appli
21		31.4	25.1	290040	8	US-10-850-586-3	Sequence 3, Appli
22	c	30.8	24.6	1493	8	US-10-739-930-436	Sequence 436, App
23	c	30.4	24.3	454	8	US-10-357-930-9645	Sequence 9645, Ap
24		30.4	24.3	541	4	US-09-925-065A-876467	Sequence 876467,
25	c	30	24.0	545	5	US-10-027-632-79040	Sequence 79040, A
26	c	30	24.0	545	5	US-10-027-632-79041	Sequence 79041, A
27	c	30	24.0	545	5	US-10-027-632-79042	Sequence 79042, A
28	c	30	24.0	545	5	US-10-027-632-79043	Sequence 79043, A
29	c	30	24.0	545	6	US-10-027-632-79040	Sequence 79040, A
30	c	30	24.0	545	6	US-10-027-632-79041	Sequence 79041, A
31	c	30	24.0	545	6	US-10-027-632-79042	Sequence 79042, A
32	c	30	24.0	545	6	US-10-027-632-79043	Sequence 79043, A
33	c	30	24.0	7005	6	US-10-369-493-26248	Sequence 26248, A
34	c	29.8	23.8	52679	5	US-10-087-192-553	Sequence 553, App
35	c	29.6	23.7	582	4	US-09-925-065A-400790	Sequence 400790,
36	c	29.6	23.7	2144	5	US-10-027-632-100413	Sequence 100413,
37	c	29.6	23.7	2144	5	US-10-027-632-103092	Sequence 103092,
38	c	29.6	23.7	2144	6	US-10-027-632-100413	Sequence 100413,
39	c	29.6	23.7	2144	6	US-10-027-632-103092	Sequence 103092,
40		29.6	23.7	2150	5	US-10-027-632-97497	Sequence 97497, A
41		29.6	23.7	2150	6	US-10-027-632-97497	Sequence 97497, A
42		29.2	23.4	474	3	US-09-864-761-11535	Sequence 11535, A
43		28.8	23.0	500	5	US-10-027-632-104434	Sequence 104434,
44		28.8	23.0	500	5	US-10-027-632-325533	Sequence 325533,
45		28.8	23.0	500	6	US-10-027-632-104434	Sequence 104434,

ALIGNMENTS

RESULT 1
US-09-875-453-9
; Sequence 9, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.

```
;  APPLICANT:  Laurance, Megan E.
;  APPLICANT:  Michelotti, Emil F.
;  APPLICANT:  Velligan, Mark D.
;  APPLICANT:  Latour, Derek R.
;  APPLICANT:  Thomas, Rita L.
;  APPLICANT:  Kongpachith, Ana
;  APPLICANT:  Sheppard, Liana T.
;  APPLICANT:  Lim, Moon Young
;  APPLICANT:  Bruice, Thomas W.
;  TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
;  FILE REFERENCE: 4600-0135.30
;  CURRENT APPLICATION NUMBER: US/09/875,453
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,549
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 2395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-875-453-9

  Query Match           89.6%;  Score 112;  DB 3;  Length 2395;
  Best Local Similarity  99.2%;  Pred. No. 4.7e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 2
US-09-909-595-10
; Sequence 10, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Scott E. Davis
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
;  FILE REFERENCE: RTS-0223
;  CURRENT APPLICATION NUMBER: US/09/909,595
;  CURRENT FILING DATE:  2001-07-18
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
;   LENGTH: 2395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1939)...(2094)
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US-09-909-595-10

Query Match 89.6%; Score 112; DB 3; Length 2395;
Best Local Similarity 99.2%; Pred. No. 4.7e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872
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RESULT 3
US-10-484-007-10
; Sequence 10, Application US/10484007
; Publication No. US20040259824A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTSP-0397
; CURRENT APPLICATION NUMBER: US/10/484,007
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/909,595
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1939)...(2094)
US-10-484-007-10

Query Match 89.6%; Score 112; DB 8; Length 2395;
Best Local Similarity 99.2%; Pred. No. 4.7e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872
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```
RESULT 4
US-10-218-654-64
; Sequence 64, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Yang, Shumin
;  APPLICANT:  Dreitz, Matthew J.
;  APPLICANT:  Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C1
;  CURRENT APPLICATION NUMBER: US/10/218,654
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (284)..(1063)
US-10-218-654-64

  Query Match             87.8%;  Score 109.8;  DB 5;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 2.6e-28;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 5
US-10-218-654-66/c
; Sequence 66, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Yang, Shumin
;  APPLICANT:  Dreitz, Matthew J.
;  APPLICANT:  Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C1
;  CURRENT APPLICATION NUMBER: US/10/218,654
;  CURRENT FILING DATE:  2002-08-13
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;  PRIOR APPLICATION NUMBER: US/09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-218-654-66

  Query Match             87.8%;  Score 109.8;  DB 5;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 2.6e-28;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| |||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db       1786 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662


RESULT 6
US-10-262-439-64
; Sequence 64, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Yang, Shumin
;  APPLICANT:  Dreitz, Matthew J.
;  APPLICANT:  Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C2
;  CURRENT APPLICATION NUMBER: US/10/262,439
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: US/09/451,527
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (284)..(1063)
US-10-262-439-64

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
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  Best Local Similarity   97.6%;  Pred. No. 2.6e-28;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| |||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         93 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy        121 CTTTG 125
              |||||
Db        213 CTTTG 217


RESULT 7
US-10-262-439-66/c
; Sequence 66, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
;  APPLICANT: Sim, Gek-Kee
;  APPLICANT:  Yang, Shumin
;  APPLICANT:  Dreitz, Matthew J.
;  APPLICANT:  Wonderling, Ramani S.
;  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES, AND USES THEREOF
;  FILE REFERENCE: IM-2-C2
;  CURRENT APPLICATION NUMBER: US/10/262,439
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: US/09/451,527
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 09/322,409
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,306
;  PRIOR FILING DATE: 1998-05-29
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-262-439-66

  Query Match             87.8%;  Score 109.8;  DB 6;  Length 1878;
  Best Local Similarity   97.6%;  Pred. No. 2.6e-28;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||| |||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1786 AAAAAAAAAAAACCTTTACGTAACTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 1667

Qy        121 CTTTG 125
              |||||
Db       1666 CTTTG 1662
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RESULT 8
US-10-311-455-1821
; Sequence 1821, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1821
;   LENGTH: 7057
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1821

  Query Match             74.9%;  Score 93.6;  DB 6;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 2.5e-22;
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  ||||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||| || |||||||||||| | |||| ||||  |||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973


RESULT 9
US-10-240-485-147
; Sequence 147, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with
;  TITLE OF INVENTION:  Metastasis
;  FILE REFERENCE: 5013.1007
;  CURRENT APPLICATION NUMBER: US/10/240,485
;  CURRENT FILING DATE:  2002-10-02
;  PRIOR APPLICATION NUMBER: PCT/EP01/03970
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: DE 10019058.8
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;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 147
;   LENGTH: 7057
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-147

  Query Match             74.9%;  Score 93.6;  DB 6;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 2.5e-22;
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                ||||||||||||  || |||||||||||  | ||||  ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973


RESULT 10
US-10-221-613-317
; Sequence 317, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, ALexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
;  FILE REFERENCE: 5013.1004
;  CURRENT APPLICATION NUMBER: US/10/221,613
;  CURRENT FILING DATE:  2002-09-13
;  PRIOR APPLICATION NUMBER: PCT/EP01/02945
;    DE 10013847.00
;    DE 10019058.8
;    DE 10019173.8
;    DE 10032529.7
;    DE 10043826.1
;  PRIOR FILING DATE: 2001-03-15
;    2000-03-15
;    2000-04-06
;    2000-04-07
;    2000-06-30
;    2000-09-01
;  NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 317
;   LENGTH: 7057
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-317

  Query Match             74.9%;  Score 93.6;  DB 7;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 2.5e-22;
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||  ||||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
                |||||||||||| || |||||||||||| | |||| ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973


RESULT 11
US-10-221-714A-323
; Sequence 323, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with
;  TITLE OF INVENTION:  tumor suppressor genes and oncogenes
;  FILE REFERENCE: 5013.1005
;  CURRENT APPLICATION NUMBER: US/10/221,714A
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/02955
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: DE 10013847.0
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 323
;   LENGTH: 7057
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-323

  Query Match             74.9%;  Score 93.6;  DB 7;  Length 7057;
  Best Local Similarity   84.7%;  Pred. No. 2.5e-22;
  Matches  105;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
```

```
              ||||| ||||||  |||||||||||||||| |||||||||||| ||||||| | |||||
Db       4850 AAAAATAAAAAATTTTTACGTAACGTTTTTGTTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||||||||||| || |||||||||||| | |||| ||||  ||||||||||||  |
Db       4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy        122 TTTG 125
              ||||
Db       4970 TTTG 4973
```

RESULT 12
US-10-311-455-1822/c
; Sequence 1822, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1822
; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1822

Query Match 67.7%; Score 84.6; DB 6; Length 7057;
Best Local Similarity 80.5%; Pred. No. 4e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||||||||| ||   | | || |||||||| ||||||||
Db       2208 AAAAACAAAAAACCTTTACGTAACGTTTTTACTAAAAAAAAAAACTACGAAACACATTTT 2149

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||  || | |   || |||||||| | |||||||||||||||| | |||  |  ||||
Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
              |||
Db       2088 TTT 2086
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RESULT 13
US-10-240-485-148/c
; Sequence 148, Application US/10240485
; Publication No. US20030148327A1

; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 148
; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-148

Query Match 67.7%; Score 84.6; DB 6; Length 7057;
Best Local Similarity 80.5%; Pred. No. 4e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||| ||   | | || |||||||| ||||||||
Db       2208 AAAAACAAAAAACCTTTACGTAACGTTTTTACTAAAAAAAAAAACTACGAAACACATTTT 2149

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||  || | |   || |||||||| | |||||||||||||||| | |||  |  ||||
Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
              |||
Db       2088 TTT 2086
```

RESULT 14
US-10-221-613-318/c
; Sequence 318, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, ALexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8

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;    DE 10032529.7
;    DE 10043826.1
;  PRIOR FILING DATE: 2001-03-15
;    2000-03-15
;    2000-04-06
;    2000-04-07
;    2000-06-30
;    2000-09-01
;  NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 318
;   LENGTH: 7057
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-318

  Query Match             67.7%;  Score 84.6;  DB 7;  Length 7057;
  Best Local Similarity   80.5%;  Pred. No. 4e-19;
  Matches   99;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||||||||| ||   | | || |||||||| ||||||||
Db       2208 AAAAACAAAAAACCTTTACGTAACGTTTTTACTAAAAAAAAAAACTACGAAACACATTTT 2149

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||  || | |   || |||||||| | |||||||||||||||| | |||  |  ||||
Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
              |||
Db       2088 TTT 2086


RESULT 15
US-10-221-714A-324/c
; Sequence 324, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with
;  TITLE OF INVENTION:  tumor suppressor genes and oncogenes
;  FILE REFERENCE: 5013.1005
;  CURRENT APPLICATION NUMBER: US/10/221,714A
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/02955
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: DE 10013847.0
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 324
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; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-324

Query Match 67.7%; Score 84.6; DB 7; Length 7057;
Best Local Similarity 80.5%; Pred. No. 4e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||||||||||  ||   | | || ||||||||  ||||||||
Db       2208 AAAAACAAAAAACCTTTACGTAACGTTTTTACTAAAAAAAAAAAACTACGAAACACATTTT 2149

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||  ||  | |   || ||||||||  | ||||||||||||||||  | |||  |  ||||
Db       2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy        122 TTT 124
              |||
Db       2088 TTT 2086
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Search completed: April 25, 2006, 12:00:54
Job time : 432 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rnpbn.

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rnpbn.

start

Go Back to previous page

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                        GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:          April 25, 2006, 10:54:00 ; Search time 359 Seconds
                                            (without alignments)
                                            1408.985 Million cell updates/sec

Title:           US-10-088-319-2_COPY_331_455
Perfect score:   125
Sequence:        1 caaaaacaaaaaacctttac.........tgagtaaggtggccactttg 125

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        9288580 seqs, 2023302648 residues

Total number of hits satisfying chosen parameters:      18577160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_NA_New:*
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                 2:  /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3:  /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4:  /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                 6:  /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
                 7:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                 9:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
                10:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
                11:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                12:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
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                15:  /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	112	89.6	6653	14	US-11-122-329-5	Sequence 5, Appli
	2	30.4	24.3	523	9	US-10-301-480-14522	Sequence 14522, A
	3	30.4	24.3	523	10	US-10-301-480-627931	Sequence 627931,
	4	30.4	24.3	525	9	US-10-301-480-14520	Sequence 14520, A
	5	30.4	24.3	525	9	US-10-301-480-14521	Sequence 14521, A
	6	30.4	24.3	525	10	US-10-301-480-627929	Sequence 627929,
	7	30.4	24.3	525	10	US-10-301-480-627930	Sequence 627930,
	8	30.4	24.3	541	6	US-09-925-065A-876467	Sequence 876467,
	9	30	24.0	525	9	US-10-301-480-14519	Sequence 14519, A
	10	30	24.0	525	10	US-10-301-480-627928	Sequence 627928,
c	11	29.6	23.7	574	10	US-10-301-480-467966	Sequence 467966,
c	12	29.6	23.7	577	10	US-10-301-480-1081375	Sequence 1081375,
c	13	29.6	23.7	582	6	US-09-925-065A-400790	Sequence 400790,
	14	28.8	23.0	92600	8	US-10-857-780-1	Sequence 1, Appli
	15	28.6	22.9	397	6	US-09-925-065A-638583	Sequence 638583,
c	16	28.6	22.9	405	9	US-10-301-480-1740	Sequence 1740, Ap
c	17	28.6	22.9	405	10	US-10-301-480-615149	Sequence 615149,
	18	28.6	22.9	3051	9	US-10-301-480-91542	Sequence 91542, A
	19	28.6	22.9	3051	9	US-10-301-480-91543	Sequence 91543, A
	20	28.6	22.9	3051	10	US-10-301-480-704951	Sequence 704951,
	21	28.6	22.9	3051	10	US-10-301-480-704952	Sequence 704952,
c	22	28.4	22.7	452	6	US-09-925-065A-360582	Sequence 360582,
c	23	28.2	22.6	470	6	US-09-925-065A-493015	Sequence 493015,
	24	28.2	22.6	581	6	US-09-925-065A-495522	Sequence 495522,
	25	28.2	22.6	581	6	US-09-925-065A-495523	Sequence 495523,
	26	28.2	22.6	599	6	US-09-925-065A-620025	Sequence 620025,
c	27	28	22.4	546	6	US-09-925-065A-833083	Sequence 833083,
c	28	28	22.4	1732	8	US-10-750-185-51775	Sequence 51775, A
c	29	28	22.4	1732	8	US-10-750-623-51775	Sequence 51775, A
	30	27.8	22.2	830	11	US-11-096-568A-29463	Sequence 29463, A
	31	27.8	22.2	947	8	US-10-750-185-60849	Sequence 60849, A
	32	27.8	22.2	947	8	US-10-750-623-60849	Sequence 60849, A
c	33	27.8	22.2	241805	8	US-10-995-561-13215	Sequence 13215, A
c	34	27.2	21.8	533	10	US-10-301-480-276541	Sequence 276541,
c	35	27.2	21.8	533	10	US-10-301-480-276543	Sequence 276543,
c	36	27.2	21.8	533	10	US-10-301-480-889950	Sequence 889950,
c	37	27.2	21.8	533	10	US-10-301-480-889952	Sequence 889952,
c	38	27.2	21.8	540	6	US-09-925-065A-186401	Sequence 186401,
c	39	27.2	21.8	540	6	US-09-925-065A-186403	Sequence 186403,
c	40	27.2	21.8	540	6	US-09-925-065A-186404	Sequence 186404,
c	41	27.2	21.8	555	10	US-10-301-480-431686	Sequence 431686,
c	42	27.2	21.8	555	10	US-10-301-480-431688	Sequence 431688,
c	43	27.2	21.8	555	10	US-10-301-480-1045095	Sequence 1045095,
c	44	27.2	21.8	555	10	US-10-301-480-1045097	Sequence 1045097,
c	45	27.2	21.8	556	6	US-09-925-065A-360583	Sequence 360583,

ALIGNMENTS

RESULT 1
US-11-122-329-5

```
; Sequence 5, Application US/11122329
; Publication No. US20060019272A1
; GENERAL INFORMATION:
;  APPLICANT: Geraci, Mark
;  APPLICANT:  Bull, Todd
;  APPLICANT:  Voelkel, Norbert
;  APPLICANT:  Coldren, Chris
;  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
;  TITLE OF INVENTION:  Expression Analysis of Peripheral Blood Cells
;  FILE REFERENCE: 2848-54
;  CURRENT APPLICATION NUMBER: US/11/122,329
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/568,129
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 6653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(6653)
;   OTHER INFORMATION: n = a,c,t,g
US-11-122-329-5

  Query Match             89.6%;  Score 112;  DB 14;  Length 6653;
  Best Local Similarity   99.2%;  Pred. No. 1.2e-27;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1750 AAAAACAAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy        122 TTTG 125
              ||||
Db       1869 TTTG 1872


RESULT 2
US-10-301-480-14522
; Sequence 14522, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14522
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;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-14522

  Query Match             24.3%;  Score 30.4;  DB 9;  Length 523;
  Best Local Similarity   55.8%;  Pred. No. 3.1;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        277 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 336

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        337 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 380


RESULT 3
US-10-301-480-627931
; Sequence 627931, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627931
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-627931

  Query Match             24.3%;  Score 30.4;  DB 10;  Length 523;
  Best Local Similarity   55.8%;  Pred. No. 3.1;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        277 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 336

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        337 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 380


RESULT 4
US-10-301-480-14520
; Sequence 14520, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
```

```
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14520
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-14520

  Query Match             24.3%;  Score 30.4;  DB 9;  Length 525;
  Best Local Similarity   55.8%;  Pred. No. 3.1;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        283 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386


RESULT 5
US-10-301-480-14521
; Sequence 14521, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14521
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-14521

  Query Match             24.3%;  Score 30.4;  DB 9;  Length 525;
  Best Local Similarity   55.8%;  Pred. No. 3.1;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        283 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
```

```
                |  | |   |    ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386


RESULT 6
US-10-301-480-627929
; Sequence 627929, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627929
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-627929

  Query Match             24.3%;  Score 30.4;  DB 10;  Length 525;
  Best Local Similarity   55.8%;  Pred. No. 3.1;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        283 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386


RESULT 7
US-10-301-480-627930
; Sequence 627930, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627930
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
```

US-10-301-480-627930

Query Match 24.3%; Score 30.4; DB 10; Length 525;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        283 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386
```

RESULT 8
US-09-925-065A-876467
; Sequence 876467, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 876467
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-876467

Query Match 24.3%; Score 30.4; DB 6; Length 541;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||||   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        304 AAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 363

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        364 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 407
```

RESULT 9
US-10-301-480-14519
; Sequence 14519, Application US/10301480
; Publication No. US20060057564A1

```
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14519
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-14519

  Query Match             24.0%;  Score 30;  DB 9;  Length 525;
  Best Local Similarity   54.8%;  Pred. No. 4.3;
  Matches   57;  Conservative    1;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||:|   ||| ||||  |   || ||  ||  | || || |   |||||||
Db        283 AAAAAAAAAARAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |  . ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386


RESULT 10
US-10-301-480-627928
; Sequence 627928, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627928
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-627928

  Query Match             24.0%;  Score 30;  DB 10;  Length 525;
  Best Local Similarity   54.8%;  Pred. No. 4.3;
  Matches   57;  Conservative    1;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||||| ||||:|   ||| ||||  |   || ||  ||  | || || |   |||||||
```

```
Db        283 AAAAAAAAAARAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCC 105
              |  | |   |    ||||| |    | ||   ||  ||   |||
Db        343 CAGGAATTAGCAAACTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386


RESULT 11
US-10-301-480-467966/c
; Sequence 467966, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 467966
;   LENGTH: 574
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-467966

  Query Match             23.7%;  Score 29.6;  DB 10;  Length 574;
  Best Local Similarity   64.7%;  Pred. No. 6;
  Matches   44;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          4 AAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
              |||  || |||  | || ||| || |||| ||| ||| |   ||| | |||| |   | |
Db        331 AAATTAAGAACGATAACTTAAGGTATTTGGTGGAAGAAATTTCTAAGCAGCAAAGCATTC 272

Qy         64 AGGAAGTG 71
              | || |||
Db        271 AAGATGTG 264


RESULT 12
US-10-301-480-1081375/c
; Sequence 1081375, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1081375
```

```
;   LENGTH: 577
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-1081375

  Query Match             23.7%;  Score 29.6;  DB 10;  Length 577;
  Best Local Similarity   64.7%;  Pred. No. 6;
  Matches   44;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          4 AAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
              |||  || |||  | || ||| || |||| ||| ||| |   ||| | |||| |   | |
Db        334 AAATTAAGAACGATAACTTAAGGTATTTGGTGGAAGAAATTTCTAAGCAGCAAAGCATTC 275

Qy         64 AGGAAGTG 71
              | || |||
Db        274 AAGATGTG 267


RESULT 13
US-09-925-065A-400790/c
; Sequence 400790, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 400790
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-400790

  Query Match             23.7%;  Score 29.6;  DB 6;  Length 582;
  Best Local Similarity   64.7%;  Pred. No. 6;
  Matches   44;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          4 AAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
              |||  || |||  | || ||| || |||| ||| ||| |   ||| | |||| |   | |
Db        339 AAATTAAGAACGATAACTTAAGGTATTTGGTGGAAGAAATTTCTAAGCAGCAAAGCATTC 280

Qy         64 AGGAAGTG 71
              | || |||
Db        279 AAGATGTG 272


RESULT 14
```

```
US-10-857-780-1
; Sequence 1, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
;  APPLICANT: ROTH, RICHARD B.
;  APPLICANT:  BRAUN, ANDREAS
;  APPLICANT:  KAMMERER, STEFAN M.
;  APPLICANT:  NELSON, MATTHEW ROBERTS
;  APPLICANT:  RENELAND, RIKARD HENRY
;  APPLICANT:  HOYAL-WRIGHTSON, CAROLYN R.
;  TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: SEQ-4069-CP
;  CURRENT APPLICATION NUMBER: US/10/857,780
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: 10/723,681
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: 60/490,234
;  PRIOR FILING DATE: 2003-07-24
;  PRIOR APPLICATION NUMBER: 60/525,239
;  PRIOR FILING DATE: 2003-11-25
;  NUMBER OF SEQ ID NOS: 4962
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 92600
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (22393)..(22394)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (24675)..(24676)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (31942)..(31942)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (32965)..(32966)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (33724)..(33724)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-1

  Query Match             23.0%;  Score 28.8;  DB 8;  Length 92600;
  Best Local Similarity   56.2%;  Pred. No. 61;
  Matches   54;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              | |||||||| || ||  |  |||   ||  | |  |  ||  | | || | | |
Db       3143 CCAAAACAAAGAAACTAAAAATAAGCATTCGGATTTGTTAGGGGGCGACAAGGGAGGCAC 3202

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTT 96
              |||||||  ||||| || |     |||| |  || |
Db       3203 TCCAGGATCTGTGGACTCCCCACTTTGTTCTGTCCT 3238
```

```
RESULT 15
US-09-925-065A-638583
; Sequence 638583, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 638583
;   LENGTH: 397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-638583

  Query Match             22.9%;  Score 28.6;  DB 6;  Length 397;
  Best Local Similarity   53.0%;  Pred. No. 12;
  Matches   61;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          7 CAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGG 66
              | ||| |  |  | |||||   |  ||   || | || ||  |  | |  ||| |  | |
Db         84 CCAAAGATATACAAGTAACCAGTAAGCACAGAAAAAAAACAGCATAACTAATTATTAAAG 143

Qy         67 AAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||||        ||| ||  || | | | |  | | ||  | || | |||| ||
Db        144 AAGTGCAAATCAAAACCATGATGAGATATCACTTTACCCCTATTAGGATGGCTAC 198


Search completed: April 25, 2006, 12:06:58
Job time : 359 secs
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SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rst.

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rst.

start

Go Back to previous page

```
                          GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:         April 25, 2006, 10:08:11 ; Search time 1987 Seconds
                                           (without alignments)
                                           2943.324 Million cell updates/sec

Title:          US-10-088-319-2_COPY_331_455
Perfect score:  125
Sequence:       1 caaaaacaaaaaacctttac.........tgagtaaggtggccactttg 125

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:      82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                1:  gb_est1:*
                2:  gb_est2:*
                3:  gb_est3:*
                4:  gb_htc:*
                5:  gb_est4:*
                6:  gb_est5:*
                7:  gb_est6:*
                8:  gb_est7:*
                9:  gb_gss1:*
                10:  gb_gss2:*
                11:  gb_gss3:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	119.2	95.4	740	7	CK834247	CK834247 4058618 B
	2	105.4	84.3	665	8	DN995162	DN995162 TC112886
	3	32.8	26.2	650	6	CA339153	CA339153 NISC_1x11
c	4	31.8	25.4	578	2	BI291532	BI291532 UI-R-DM0-
	5	31.6	25.3	480	10	CE391194	CE391194 tigr-gss-
c	6	31.4	25.1	788	9	BZ459393	BZ459393 BONIE51TF
c	7	31.4	25.1	1032	11	CNS05L3M	AL342283 Tetraodon
c	8	31.2	25.0	529	2	BI291766	BI291766 UI-R-DM0-
	9	31.2	25.0	579	7	CF918988	CF918988 Bflor531.
c	10	31.2	25.0	627	2	BI285373	BI285373 UI-R-DB0-
c	11	31.2	25.0	630	2	BI279004	BI279004 UI-R-DB0-
c	12	31.2	25.0	655	2	BI285082	BI285082 UI-R-DB0-
	13	31	24.8	669	10	CW685817	CW685817 OG_BBa004
c	14	30.8	24.6	422	3	BI527837	BI527837 1024084H1
c	15	30.8	24.6	452	3	BI999848	BI999848 1031079E0
c	16	30.8	24.6	508	3	BI995666	BI995666 1031029D0
c	17	30.8	24.6	553	5	BU652076	BU652076 1112097D0
c	18	30.8	24.6	601	3	BM003194	BM003194 1031109A1
c	19	30.8	24.6	613	3	BI723641	BI723641 1031067D0
c	20	30.8	24.6	638	3	BI723640	BI723640 1031067D0
c	21	30.8	24.6	639	3	BI724908	BI724908 1031075H0
c	22	30.8	24.6	747	2	BF864016	BF864016 963048D09
c	23	30.8	24.6	801	2	BG844410	BG844410 1024006C1
c	24	30.8	24.6	1027	9	CC258992	CC258992 CH261-52F
c	25	30.8	24.6	1427	4	CNS0A2EV	BX827719 Arabidops
c	26	30.6	24.5	432	9	BZ768094	BZ768094 SALK_1397
c	27	30.6	24.5	474	6	CB407550	CB407550 IPG030C06
	28	30.6	24.5	478	7	CF962820	CF962820 8997rsice
	29	30.6	24.5	634	5	BU437831	BU437831 604145016
c	30	30.6	24.5	1017	3	BQ050581	BQ050581 AGENCOURT
	31	30.6	24.5	1550	10	CL019408	CL019408 CH216-5D1
	32	30.4	24.3	495	7	CN679199	CN679199 E0121C11-
	33	30.4	24.3	552	7	CN681667	CN681667 E0153F05-
c	34	30.4	24.3	594	3	BJ017277	BJ017277 BJ017277
c	35	30.4	24.3	741	8	DR103237	DR103237 JHU027E09
c	36	30.4	24.3	866	7	CN172789	CN172789 AGENCOURT
c	37	30.2	24.2	433	9	AZ618267	AZ618267 1M0449I20
c	38	30.2	24.2	479	9	BZ720597	BZ720597 PUDAU30TB
	39	30.2	24.2	738	9	BZ720601	BZ720601 PUDAU30TD
c	40	30.2	24.2	786	6	CB308629	CB308629 AGENCOURT
	41	30.2	24.2	864	6	CD379455	CD379455 PTMM04624
c	42	30.2	24.2	951	7	CO028574	CO028574 EST806958
c	43	30	24.0	665	5	BU429602	BU429602 UI-HF-BN0
	44	29.8	23.8	431	5	BW514275	BW514275 BW514275
c	45	29.8	23.8	496	6	CA626341	CA626341 wl1n.pk01

ALIGNMENTS

RESULT 1
CK834247
LOCUS CK834247 740 bp mRNA linear EST 04-MAR-2004
DEFINITION 4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA sequence.
ACCESSION CK834247

```
VERSION     CK834247.1  GI:45064536
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
  TITLE     Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt '' -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 2  row: M  column: 16
            Seq primer: CCTATTTAGGTGACACTATAGAAC
            High quality sequence stop: 740.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="8BOV_2M16"
                     /sex="Female"
                     /tissue_type="Epithelial, Muscle"
                     /dev_stage="Lactating, Neonatal"
                     /lab_host="DH10B TonA"
                     /clone_lib="BARC 8BOV"
                     /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
                     NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
                     library in pCMVsport6.1, constructed from equimolar mRNA
                     pools derived from 5 sources, 4 lactating intestinal, 1
                     neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                     Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                     Duodenum, Jejunum, Distal Ileum"
ORIGIN

  Query Match             95.4%;  Score 119.2;  DB 7;  Length 740;
  Best Local Similarity   97.6%;  Pred. No. 8.5e-29;
  Matches  121;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db        102 AAAAACAAAAAACCTTTACGTAACTTTTTTGCTGGGAGAGAAGACTGCGAAGCACATTTT 161

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        162 CCAGGAAGTGTGGGCTGCGACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 221

Qy        122 TTTG 125
              ||||
```

```
Db        222 TTTG 225


RESULT 2
DN995162
LOCUS       DN995162                 665 bp    mRNA    linear   EST 17-MAY-2005
DEFINITION  TC112886 Human adult whole brain, large insert, pCMV expression
            library Homo sapiens cDNA clone TC112886 5' similar to Homo sapiens
            CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)
            (CD40LG), mRNA sequence.
ACCESSION   DN995162
VERSION     DN995162.1  GI:66254993
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 665)
  AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
  TITLE     High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. ( www.origene.com )
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES             Location/Qualifiers
     source          1. .665
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TC112886"
                     /tissue_type="Whole brain"
                     /clone_lib="Human adult whole brain, large insert, pCMV
                     expression library"
                     /note="Organ: Brain; Vector: pCMV6-XL5; Site_1: EcoR1;
                     Site_2: Xho1/Sal1 compatible end ligatio; Oligo-dT primed
                     reverse transcription optimized for large and GC rich mRNA
                     transcripts, cDNA size selection, optimized ligation for
                     large inserts into mammalian expression vector, random
                     clones selected for end sequence verification of
                     full-length genes"
ORIGIN

  Query Match             84.3%;  Score 105.4;  DB 8;  Length 665;
```

```
  Best Local Similarity   99.1%;  Pred. No. 3.5e-24;
  Matches  106;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 ACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTG 78
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 AGGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTG 64

Qy         79 CAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACTTTG 125
              |||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCACTTTG 111


RESULT 3
CA339153
LOCUS       CA339153                650 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  NISC_1x11d02.y1 NCI_CGAP_Pr51 Rattus norvegicus cDNA clone
            IMAGE:5621810 5', mRNA sequence.
ACCESSION   CA339153
VERSION     CA339153.1  GI:24557251
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 650)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM12446  row: H  column: 3
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .650
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:5621810"
                     /sex="male"
                     /tissue_type="pool of ventral and dorsolateral prostate"
                     /dev_stage="adult, 10 week"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Pr51"
                     /note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
                     NotI; Site_2: EcoRV; Cloned unidirectionally. Primer:
                     Oligo dT. Pool of 2 primary libraries: NCI_CGAP_Pr46
                     (ventral prostate from 10 wk male, average insert size 2
                     kb) and NCI_CGAP_Pr47 (dorsolateral prostate from 10 wk
                     male, average insert size 2 kb). Constructed by
                     Invitrogen. Note: this is a NCI_CGAP Library."
ORIGIN
```

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  Query Match             26.2%;  Score 32.8;  DB 6;  Length 650;
  Best Local Similarity   54.0%;  Pred. No. 8.1;
  Matches   67;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||  |   |   || | ||  |||    | || ||| || ||||||   ||||   ||
Db        209 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 268

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               |||  |   |   ||||| || ||   ||   | | |  | ||| | || ||    ||
Db        269 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAAGCAAAACAGCATG 328

Qy        122 TTTG 125
              ||||
Db        329 TTTG 332


RESULT 4
BI291532/c
LOCUS       BI291532                 578 bp    mRNA    linear   EST 19-JUL-2001
DEFINITION  UI-R-DM0-cis-n-19-0-UI.s1 UI-R-DM0 Rattus norvegicus cDNA clone
            UI-R-DM0-cis-n-19-0-UI 3', mRNA sequence.
ACCESSION   BI291532
VERSION     BI291532.1  GI:14951161
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized rat prostate library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com) The following repetitive
            elements were found in this cDNA sequence: 1-21,
            >AT_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .578
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
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/clone="UI-R-DM0-cis-n-19-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-DM0"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DM0 library is a non-normalized Rat Prostate library constructed in pT3T7 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag CCAGG between the Not I cloning site and dT18 stretch.
TAG_TISSUE=rat prostate
TAG_LIB=UI-R-DM0
TAG_SEQ=CCAGG"

ORIGIN

Query Match 25.4%; Score 31.8; DB 2; Length 578;
Best Local Similarity 53.2%; Pred. No. 17;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| |  |   || | ||  |||    | || ||| || ||||||   ||||   ||
Db        537 AAACAACAGTGACTTGTATNTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 478

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               ||| |  |   ||||| || ||   ||   | | |  | ||| |  | ||    ||
Db        477 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 418

Qy        122 TTTG 125
              ||||
Db        417 TTTG 414
```

RESULT 5
CE391194
LOCUS CE391194 480 bp DNA linear GSS 27-SEP-2003
DEFINITION tigr-gss-dog-17000334460145 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE391194
VERSION CE391194.1 GI:36630810
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 480)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org

```
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             25.3%;  Score 31.6;  DB 10;  Length 480;
  Best Local Similarity   55.5%;  Pred. No. 19;
  Matches   61;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| | | | || |||||   ||  |||||  |   || ||| |||  | |  || |||
Db          7 AAATAAATAGAATCTTTAAAAAAATTTTTTTTTTCAAGTGAAAACTTTGGAAAACTTTTA 66

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTA 111
              || |  |    ||||   |  | ||       |||||  | | ||||| |
Db         67 CCTGACATCAGGGGCATGACAGGTTCAAAATACTTAAAGACTTCTGAGAA 116


RESULT 6
BZ459393/c
LOCUS       BZ459393                 788 bp    DNA     linear   GSS 13-DEC-2002
DEFINITION  BONIE51TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONIE51,
            genomic survey sequence.
ACCESSION   BZ459393
VERSION     BZ459393.1  GI:26740861
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
   PUBMED   15805490
COMMENT     Other_GSSs: BONIE51TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .788
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
```

/clone="BONIE51"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match 25.1%; Score 31.4; DB 9; Length 788;
Best Local Similarity 61.7%; Pred. No. 25;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

```
Qy          1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
              ||||  || |||  ||||| ||   || ||     ||||||   ||   |||| ||||
Db        710 CAAACGCATAAATTCTTTATGTGGAGTATTCCTATGGAGAGGTAACATTGAAGAACATCA 651

Qy         61 TCCAGGAAGTGTGGGCTGCAA 81
              | |||  || ||| | || ||
Db        650 TACAGCGAGGGTGAGTTGGAA 630
```

RESULT 7
CNS05L3M/c
LOCUS CNS05L3M 1032 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 051F03 of library A from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL342283
VERSION AL342283.1 GI:8236041
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
PUBMED 10899143
REFERENCE 3 (bases 1 to 1032)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers

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     source          1. .1032
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="051F03"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C0AA051CC02C1
                     end : T7"
ORIGIN

  Query Match             25.1%;  Score 31.4;  DB 11;  Length 1032;
  Best Local Similarity   51.0%;  Pred. No. 27;
  Matches   53;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          4 AAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
              ||  ||||| ||  || | |    |||| |  |     || |  |   |   |||||||
Db        619 AAGGAAAAANCCCNTATGAAGTCNTTTTTCANGNNNGNAAAAANANNCANNNCATTTTCT 560

Qy         64 AGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTG 107
                 |  ||| | ||   ||  | |||    | || |  | | |||
Db        559 CTGTTGTGAGAGCCTAAAAAAATGTATCATGTTTAAAATTNCTG 516


RESULT 8
BI291766/c
LOCUS       BI291766                529 bp    mRNA    linear   EST 19-JUL-2001
DEFINITION  UI-R-DM0-cis-n-18-0-UI.s1 UI-R-DM0 Rattus norvegicus cDNA clone
            UI-R-DM0-cis-n-18-0-UI 3', mRNA sequence.
ACCESSION   BI291766
VERSION     BI291766.1  GI:14951628
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized rat prostate library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .529
```

```
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DM0-cis-n-18-0-UI"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-DM0"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DM0
                     library is a non-normalized Rat Prostate library
                     constructed in pT3T7 PAC vector according to the procedure
                     described by Bonaldo, Lennon & Soares (Genome Research
                     Genome 6: 791-806, 1996). The oligonucleotide used to
                     prime first strand synthesis contained the sequence tag
                     CCAGG between the Not I cloning site and dT18 stretch.
                     TAG_TISSUE=rat prostate
                     TAG_LIB=UI-R-DM0
                     TAG_SEQ=CCAGG"
ORIGIN

  Query Match           25.0%;  Score 31.2;  DB 2;  Length 529;
  Best Local Similarity   53.2%;  Pred. No. 26;
  Matches   66;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| |  |   || | ||  |||    | || ||| || ||||||   ||||   ||
Db        527 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 468

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               ||| |  |   ||||| || ||   ||   | | |  | ||| |  | ||    ||
Db        467 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 408

Qy        122 TTTG 125
              ||||
Db        407 TTTG 404


RESULT 9
CF918988
LOCUS       CF918988                579 bp    mRNA    linear   EST 05-NOV-2003
DEFINITION  Bflor531.000073 Amphioxus 26 hrs cDNA library (Name convention:
            BFL26 or MPMGp531) Branchiostoma floridae cDNA clone
            MPMGp531J1510;BFL26_10J15 5', mRNA sequence.
ACCESSION   CF918988
VERSION     CF918988.1  GI:38190190
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J.,
            Herwig,R., Vingron,M. and Lehrach,H.
  TITLE     New evidence for genome-wide duplications at the origin of
            vertebrates using an amphioxus gene set and completed animal
            genomes
  JOURNAL   Genome Res. 13 (6A), 1056-1066 (2003)
   PUBMED   12799346
COMMENT     Contact: Panopoulou G
            laboratory 145, dept.Lehrach
```

Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of all clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at http://www.molgen.mpg.de/amphioxus.
Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de).
PCR PRimers
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
Insert Length: 1200 Std Error: 200.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 579.

FEATURES Location/Qualifiers
source 1. .579
/organism="Branchiostoma floridae"
/mol_type="mRNA"
/strain="wild type"
/db_xref="taxon:7739"
/clone="MPMGp531J1510;BFL26_10J15"
/tissue_type="whole embryo"
/dev_stage="26 hrs (neurula stage)"
/lab_host="Escherichia coli, XL1 blue"
/clone_lib="Amphioxus 26 hrs cDNA library (Name convention: BFL26 or MPMGp531)"
/note="Vector: pSport1; Site_1: SalI, KpnI, EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC (T)15-3' and a SalI 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."

ORIGIN

Query Match 25.0%; Score 31.2; DB 7; Length 579;
Best Local Similarity 57.0%; Pred. No. 27;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```
Qy          3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
              ||   | | || || ||   |    |||| ||   ||  | | ||  |||  | |  |||
Db        339 AATTGACATAAGCTGTAGACACTTATTTTTCTCCAAGGCAGGTCTTTGAATGAAACGTTC 398

Qy         63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAA 102
                || ||| | || | | || ||   || ||| ||||| ||
Db        399 AAGCAAGAGAGGACAGAAAAGAAGCTGAGCTTTTAACAAA 438
```

RESULT 10
BI285373/c
LOCUS BI285373 627 bp mRNA linear EST 19-JUL-2001
DEFINITION UI-R-DB0-byz-c-11-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone UI-R-DB0-byz-c-11-0-UI 3', mRNA sequence.
ACCESSION BI285373

```
VERSION     BI285373.1  GI:14938944
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 627)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized bladder library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .627
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DB0-byz-c-11-0-UI"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-DB0"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
                     library is a non-normalized library constructed from rat
                     bladder tissue. For a detailed description of the library
                     from which this clone was derived, please visit our web
                     site at ratest.eng.uiowa.edu. The subtraction has been
                     previously described in (Bonaldo, Lennon and Soares,
                     Genome Research 6:791-806, 1996)
                     TAG_TISSUE=bladder
                     TAG_LIB=UI-R-DB0
                     TAG_SEQ=AGC"
ORIGIN

  Query Match             25.0%;  Score 31.2;  DB 2;  Length 627;
  Best Local Similarity   53.2%;  Pred. No. 28;
  Matches   66;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              |||  |   |   ||  |  ||  |||     | ||  |||  ||  ||||||   ||||   ||
Db        525 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 466
```

```
Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
              ||| |  |   ||||| || ||   ||   | | |  | ||| |  | ||    ||
Db        465 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 406

Qy        122 TTTG 125
              ||||
Db        405 TTTG 402


RESULT 11
BI279004/c
LOCUS       BI279004                 630 bp    mRNA    linear   EST 19-JUL-2001
DEFINITION  UI-R-DB0-byt-h-12-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone
            UI-R-DB0-byt-h-12-0-UI 3', mRNA sequence.
ACCESSION   BI279004
VERSION     BI279004.1  GI:14926402
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized bladder library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DB0-byt-h-12-0-UI"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-DB0"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
                     library is a non-normalized library constructed from rat
                     bladder tissue. For a detailed description of the library
                     from which this clone was derived, please visit our web
                     site at ratest.eng.uiowa.edu. The subtraction has been
```

previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_TISSUE=bladder
TAG_LIB=UI-R-DB0
TAG_SEQ=AGC"
ORIGIN

Query Match 25.0%; Score 31.2; DB 2; Length 630;
Best Local Similarity 53.2%; Pred. No. 28;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```
Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| |  |   || | ||  |||    | || ||| || ||||||  ||||   ||
Db        526 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 467

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               ||| |  |   ||||| || ||   ||   | | |  | ||| |  | ||    ||
Db        466 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 407

Qy        122 TTTG 125
              ||||
Db        406 TTTG 403
```

RESULT 12
BI285082/c
LOCUS BI285082 655 bp mRNA linear EST 19-JUL-2001
DEFINITION UI-R-DB0-byw-a-02-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone UI-R-DB0-byw-a-02-0-UI 3', mRNA sequence.
ACCESSION BI285082
VERSION BI285082.1 GI:14938372
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 655)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized bladder library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21,
>AT_rich#Low_complexity
Seq primer: M13 Forward

```
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DB0-byw-a-02-0-UI"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-DB0"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
                     library is a non-normalized library constructed from rat
                     bladder tissue. For a detailed description of the library
                     from which this clone was derived, please visit our web
                     site at ratest.eng.uiowa.edu. The subtraction has been
                     previously described in (Bonaldo, Lennon and Soares,
                     Genome Research 6:791-806, 1996)
                     TAG_TISSUE=bladder
                     TAG_LIB=UI-R-DB0
                     TAG_SEQ=AGC"
ORIGIN

  Query Match           25.0%;  Score 31.2;  DB 2;  Length 655;
  Best Local Similarity  53.2%;  Pred. No. 28;
  Matches   66;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              ||| |  |   || | ||  |||    | || ||| || ||||||   ||||   ||
Db        537 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 478

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
               ||| |  |   ||||| || ||  ||   | | |  | ||| |  | ||    ||
Db        477 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 418

Qy        122 TTTG 125
              ||||
Db        417 TTTG 414


RESULT 13
CW685817
LOCUS       CW685817                669 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  OG_BBa0044A23.f OG_BBa Oryza glaberrima genomic clone OG_BBa0044A23
            5', genomic survey sequence.
ACCESSION   CW685817
VERSION     CW685817.1  GI:55155379
KEYWORDS    GSS.
SOURCE      Oryza glaberrima (African rice)
  ORGANISM  Oryza glaberrima
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K.,
            Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
            and Wing,R.
  TITLE     OMAP
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
```

```
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0044  row: A  column: 23
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Oryza glaberrima"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4538"
                     /clone="OG_BBa0044A23"
                     /tissue_type="young leaves"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OG_BBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             24.8%;  Score 31;  DB 10;  Length 669;
  Best Local Similarity   59.8%;  Pred. No. 33;
  Matches   52;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
              | ||||||| || || || |  |  |||||   | | | | | | || |||| || |||
Db        161 AGAAACAAACAAACTATAGGACATCTTTTTTTAGAGCGGGTAAAGTATGAAGGACTTTTG 220

Qy         62 CCAGGAAGTGTGGGCTGCAACGATTGT 88
                | || |   || | |  | | || ||
Db        221 ACTGGGATCCTGTGGTAAAGCAATAGT 247


RESULT 14
BI527837/c
LOCUS       BI527837                 422 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  1024084H12.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
            Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BI527837
VERSION     BI527837.1  GI:15368411
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
            Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1024b
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
```

```
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES              Location/Qualifiers
     source           1. .422
                      /organism="Chlamydomonas reinhardtii"
                      /mol_type="mRNA"
                      /strain="CC-1690 wild type mt+ 21gr"
                      /db_xref="taxon:3055"
                      /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                      II"
                      /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                      XhoI; This library, constructed by John Davies and Jeffrey
                      McDermott, combines cDNAs from CC-1690 cells grown to
                      mid-log phase in TAP (acetate-containing) medium in the
                      light, TAP medium in the dark, HS (minimal) medium in
                      ambient levels of CO2 and HS medium bubbled with 5% CO2.
                      PolyA mRNA was purified from each sample, pooled and cDNA
                      synthesized. The cDNA was directionally cloned into lambda
                      ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
                      pBluescript II SK- plasmids were excised from the lambda
                      ZAP clones by superinfection with ExAssist (Stratagene)
                      phage. The library was normalized using method 4 described
                      in Bonaldo et al (1996) Genome Research 6: 791-806."
ORIGIN

  Query Match           24.6%;  Score 30.8;  DB 3;  Length 422;
  Best Local Similarity  70.7%;  Pred. No. 34;
  Matches   41;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGC 118
              ||  || ||  |||| |||| ||  ||||||||||  ||   || || || |||||||
Db        264 TCATGGCAGCATGGGATGCACCGCGTGTGCGCTCTGCACACGTCGTGGGTGAGGTGGC 207


RESULT 15
BI999848/c
LOCUS       BI999848                452 bp    mRNA    linear   EST 25-OCT-2001
DEFINITION  1031079E03.x2 C. reinhardtii CC-1690, Stress II (normalized),
            Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BI999848
VERSION     BI999848.1  GI:16434622
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
            Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1031
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Charles Hauser
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            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES              Location/Qualifiers
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                     /organism="Chlamydomonas reinhardtii"
                     /mol_type="mRNA"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, Stress II
                     (normalized), Lambda Zap II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; Stress condition II library, constructed by John
                     Davies and Jeffrey McDermott, combines cDNAs from CC-1690
                     cells grown to mid-log phase in TAP (NH4+ - containing)
                     and shifted to TAP - NO3- (24hrs); H2 production
                     conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant
                     Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
                     sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     Zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
                     sites. pBluescript II SK- plasmids were excised from the
                     lambda ZAP clones by superinfection with ExAssist
                     (Stratagene) phage. The library was normalized using
                     method 4 described in Bonaldo et al., (1996) Genome
                     Research 6: 791-806."
ORIGIN

  Query Match             24.6%;  Score 30.8;  DB 3;  Length 452;
  Best Local Similarity   70.7%;  Pred. No. 35;
  Matches   41;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

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